

FIG. 1

1
GAATTCC GACCGCAGAC

18
ATG AAA CTT GTC TTC CTC GTC CTG CTG TTC CTC GGG GCC CTC GGA CTC
met lys leu val phe leu val leu leu phe leu gly ala leu gly leu
1

66
TGT CTG GCT GGC CGT AGG AGA AGG AGT GTT CAG TGG TGC ACC GTA TCC
cys leu ala gly arg arg arg arg ser val gln trp cys thr val ser
17

114
CAA CCC GAG GCC ACA AAA TGC TTC CAA TGG CAA AGG AAT ATG AGA AGA
gln pro glu ala thr lys cys phe gln trp gln arg asn met arg arg
33

162
GTG CGT GGC CCT CCT GTC AGC TGC ATA AAG AGA GAC TCC CCC ATC CAG
val arg gly pro pro val ser cys ile lys arg asp ser pro ile gln
49

210
TGT ATC CAG GCC ATT GCG GAA AAC AGG GCC GAT GCT GTG ACC CTT GAT
cys ile gln ala ile ala glu asn arg ala asp ala val thr leu asp
65

258
GGT GGT TTC ATA TAC GAG GCA GGC CTG GCC CCC TAC AAA CTC CGA CCT
gly gly phe ile tyr glu ala gly leu ala pro tyr lys leu arg pro
81

306
GTA GCG GCG GAA GTC TAC GGG ACC GAA AGA CAG CCA CGA ACT CAC TAT
val ala ala glu val tyr gly thr glu arg gln pro arg thr his tyr
97

354
TAT GCC GTG GCT GIG GTG AAG AAG GGC GGC AGC TTT CAG CTG AAC GAA
tyr ala val ala val val lys lys gly gly ser phe gln leu asn glu
113

402
CTG CAA GGT CTG AAG TCC TGC CAC ACA GGC CTT CGC AGG ACC GCT GGA
leu gln gly leu lys ser cys his thr gly leu arg arg thr ala gly
129

450
TGG AAT GTG CCT ATA GGG ACA CTT CGT CCA TTC TTG AAT TGG ACG GGT
trp asn val pro ile gly thr leu arg pro phe leu asn trp thr gly
145

FIG. 2A

498
 CCA CCT GAG CCC ATT GAG GCA GCT GTG GCC AGG TTC TTC TCA GCC AGC
 pro pro glu pro ile glu ala ala val ala-arg phe phe ser ala ser
 161
 546
 TGT GTT CCC GGT GCA GAT AAA GGA CAG TTC CCC AAC CTG TCT CGC CTG
 cys val pro gly ala asp lys gly gln phe pro asn leu cys arg leu
 177
 594
 TGT GCG GGG ACA GGG GAA AAC AAA TGT GCC TTC TCC TCC CAG GAA CCG
 cys ala gly thr gly glu asn lys cys ala phe ser ser gln glu pro
 193
 642
 TAC TTC AGC TAC TCT GGT GCC TTC AAG TGT CTG AGA GAC GGG GCT GGA
 tyr phe ser tyr ser gly ala phe lys cys leu arg asp gly ala gly
 209
 690
 GAC GTG GCT TTT ATC AGA GAG AGC ACA GTG TTT GAG GAC CTG TCA GAC
 asp val ala phe ile arg glu ser thr val phe glu asp leu ser asp
 225
 738
 GAG GCT GAA AGG GAC GAG TAT GAG TTA CTC TGC CCA GAC AAC ACT CGG
 glu ala glu arg asp glu tyr glu leu leu cys pro asp asn thr arg
 241
 786
 AAG CCA GTG GAC AAG TTC AAA GAC TGC CAT CTG GCC CGG GTC CCT TCT
 lys pro val asp lys phe lys asp cys his leu ala arg val pro ser
 257
 834
 CAT GCC GTT GTG GCA CGA AGT GTC AAT GGC AAG GAG GAT GCC ATC TGG
 his ala val val ala arg ser val asn gly lys glu asp ala ile trp
 273
 882
 AAT CTT CTC CGC CAG GCA CAG GAA AAG TTT GGA AAG GAC AAG TCA CCG
 asn leu leu arg gln ala gln gln lys phe gly lys asp lys ser pro
 289
 930
 AAA TTC CAG CTC TTT GGC TCC GCT AGT GGG CAG AAA GAT CTG CTG TTC
 lys phe gln leu phe gly ser pro ser gly gln lys asp leu leu phe
 305
 978
 AAG GAC TCT GCC ATT GGG TTT TCG AGG CTG CCC CCG AGG ATA GAT TCT
 lys asp ser ala ile gly phe ser arg val pro pro arg ile asp ser
 321
 1026
 GGG CTG TAC CTT GGC TCC GCC TAC TTC ACT GCC ATC CAG AAC TTG AGG
 gly leu tyr leu gly ser gly tyr phe thr ala ile gln asn leu arg
 337

FIG. 2B

1074
 AAA AGT GAG GAG GAA GTG GCT GCC CGG CGT GCG CGG GTC GTG TGG TGT
 lys ser glu glu glu val ala ala arg arg ala arg val val trp cys
 353
 1122
 GCG GTG GGC GAG CAG GAG CTG CGC AAG TGT AAC CAG TGG AGT GGC TTG
 ala val gly glu gln glu leu arg lys cys asn gln trp ser gly leu
 369
 1170
 AGC GAA GGC AGC GTG ACC TGC TCC TCG GCC TCC ACC ACA GAG GAC TGC
 ser glu gly ser val thr cys ser ser ala ser thr thr glu asp cys
 385
 1218
 ATC GCC CTG GTG CTG AAA GGA GAA GCT GAT GCC ATG AGT TTG GAT GGA
 ile ala leu val leu lys gly glu ala asp ala met ser leu asp gly
 401
 1266
 GGA TAT GTG TAC ACT GCA GGC AAA TGT GGT TTG GTG CCT GTC CTG GCA
 gly tyr val tyr thr ala gly lys cys gly leu val pro val leu ala
 417
 1314
 GAG AAC TAC AAA TCC CAA CAA AGC AGT GAC CCT GAT CCT AAC TGT GTG
 glu asn tyr lys ser gln gln ser ser asp pro asp pro asn cys val
 433
 1362
 GAT AGA CCT GTG GAA GGA TAT CTT GCT GTG GCG GTG GTT AGG AGA TCA
 asp arg pro val glu gly tyr leu ala val ala val val arg arg ser
 449
 1410
 GAC ACT AGC CTT ACC TGG AAC TCT GTG AAA GGC AAG AAG TCC TGC CAC
 asp thr ser leu thr trp asn ser val lys gly lys lys ser cys his
 465
 1458
 ACC GCC GTG GAC AGG ACT GCA GGC TGG AAT ATC CCC ATG GGC CTG CTC
 thr ala val asp arg thr ala gly trp asn ile pro met gly leu leu
 481
 1506
 TTC AAC CAG ACG GGC TCC TGC AAA TTT GAT GAA TAT TTC AGT CAA AGC
 phe asn gln thr gly ser cys lys phe asp glu tyr phe ser gln ser
 497
 1554
 TGT GCC CCT GGG TCT GAC CCG AGA TCT AAT CTC TGT GCT CTG TGT ATT
 cys ala pro gly ser asp pro arg ser asn leu cys ala leu cys ile
 513
 1602
 GGC GAC GAG CAG GGT GAG AAT AAG TGC GTG CCC AAC AGC AAT GAG AGA
 gly asp glu gln gly glu asn lys cys val pro asn ser asn glu arg
 529

FIG. 2C

1650
TAC TAC GGC TAC ACT GGG GCT TTC CGG TGC CTG GCT GAG AAT GCT GGA
tyr tyr gly tyr thr gly ala phe arg cys leu ala glu asn ala gly
545

1698
GAC GTT GCA TTT GTG AAA GAT GTC ACT GTC TTG CAG AAC ACT GAT GGA
asp val ala phe val lys asp val thr val leu gln asn thr asp gly
561

1746
AAT AAC AAT GAG GCA TGG GCT AAG GAT TTG AAG CTG GCA GAC TTT GCG
asn asn asn glu ala trp ala lys asp leu lys leu ala asp phe ala
577

1794
CTG CTG TGC CTC GAT GGC AAA CGG AAG CCT GTG ACT GAG GCT AGA AGC
leu leu cys leu asp gly lys arg lys pro val thr glu ala arg ser
593

1842
TSC CAT CTT GCC ATG GCC CCG AAT CAT GCC GTG GTG TCT CGG ATG GAT
cys his leu ala met ala pro asn his ala val val ser arg met asp
609

1890
AAG GTG GAA CGC CTG AAA CAG GTG CTG CTC CAC CAA CAG GCT AAA TTT
lys val glu arg leu lys gln val leu leu his gln gln ala lys phe
625

1938
GGG AGA AAT GGA TCT GAC TGC CCG GAC AAG TTT TGC TTA TTC CAG TCT
gly arg asn gly ser asp cys pro asp lys phe cys leu phe gln ser
641

1986
GAA ACC AAA AAC CTT CTG TTC AAT GAC AAC ACT GAG TGT CTG GCC AGA
glu thr lys asn leu leu phe asn asp asn thr glu cys leu ala arg
657

2034
CTC CAT GGC AAA ACA ACA TAT GAA AAA TAT TTG GGA CCA CAG TAT GTC
leu his gly lys thr thr tyr glu lys tyr leu gly pro gln tyr val
673

2082
GCA GGC ATT ACT AAT CTG AAA AAG TGC TCA ACC TCC CCC CTC CTG GAA
ala gly ile thr asn leu lys lys cys ser thr ser pro leu leu glu
689

2130
GCC TGT GAA TTC CTC AGG AAG TAA
ala cys glu phe leu arg lys *** ACCGAA GAAGATGGCC CAGCTCCCCA
705

2180
AGAAAGCCTC AGCCATTAC TGCCCCCAGC TCTTCTCCCC AGGTGTGTIG GGGCCTTGCC

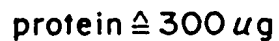
2240
TCCCCTGCTG AAGGTGGGA TTGCCCATCC ATCTGCTTAC AATTCCCTGC TGTCGTCTTA

2300
GCAAGAAGTA AAATGAGAAA TTTTGTGAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA

FIG. 2D

MEDIUM	CELL LYSATES
--------	--------------

CONTROL



HUMAN
LACTOFERRIN

FIG. 3

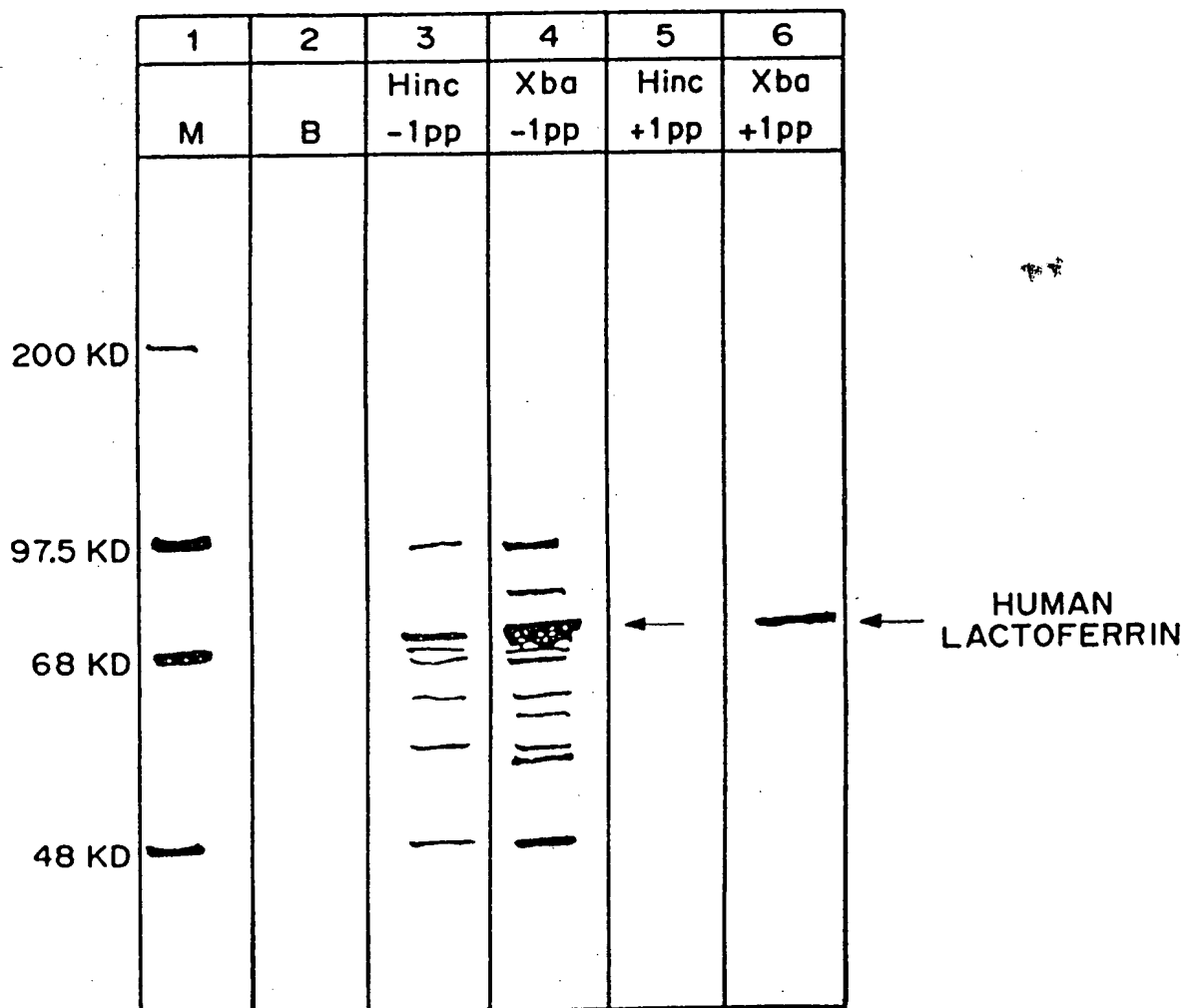


FIG.4

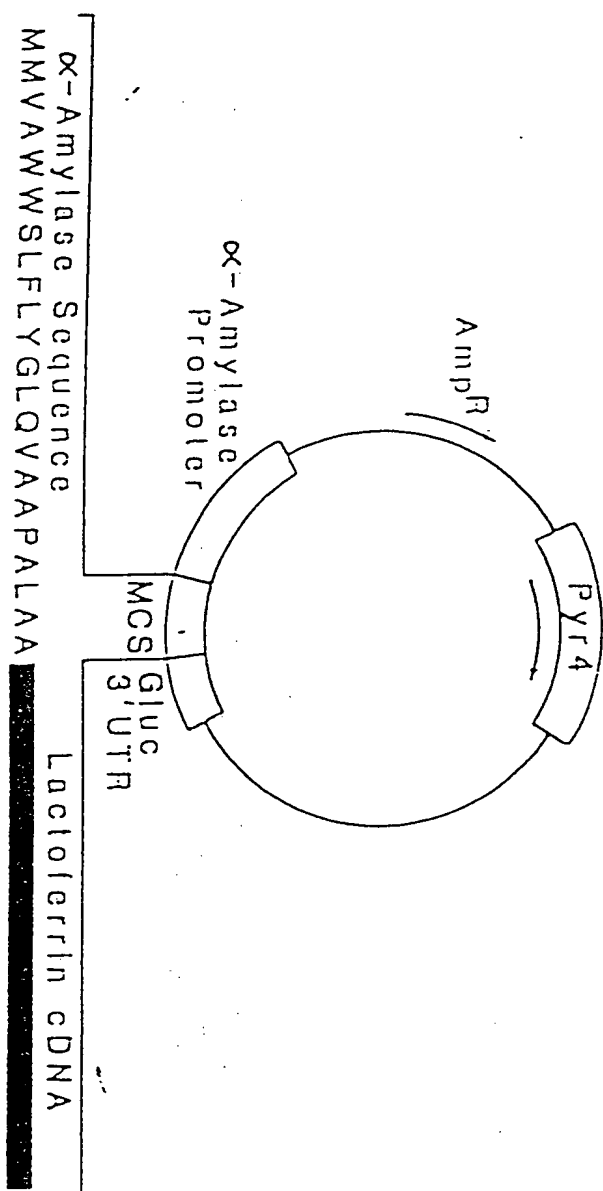


FIG. 5

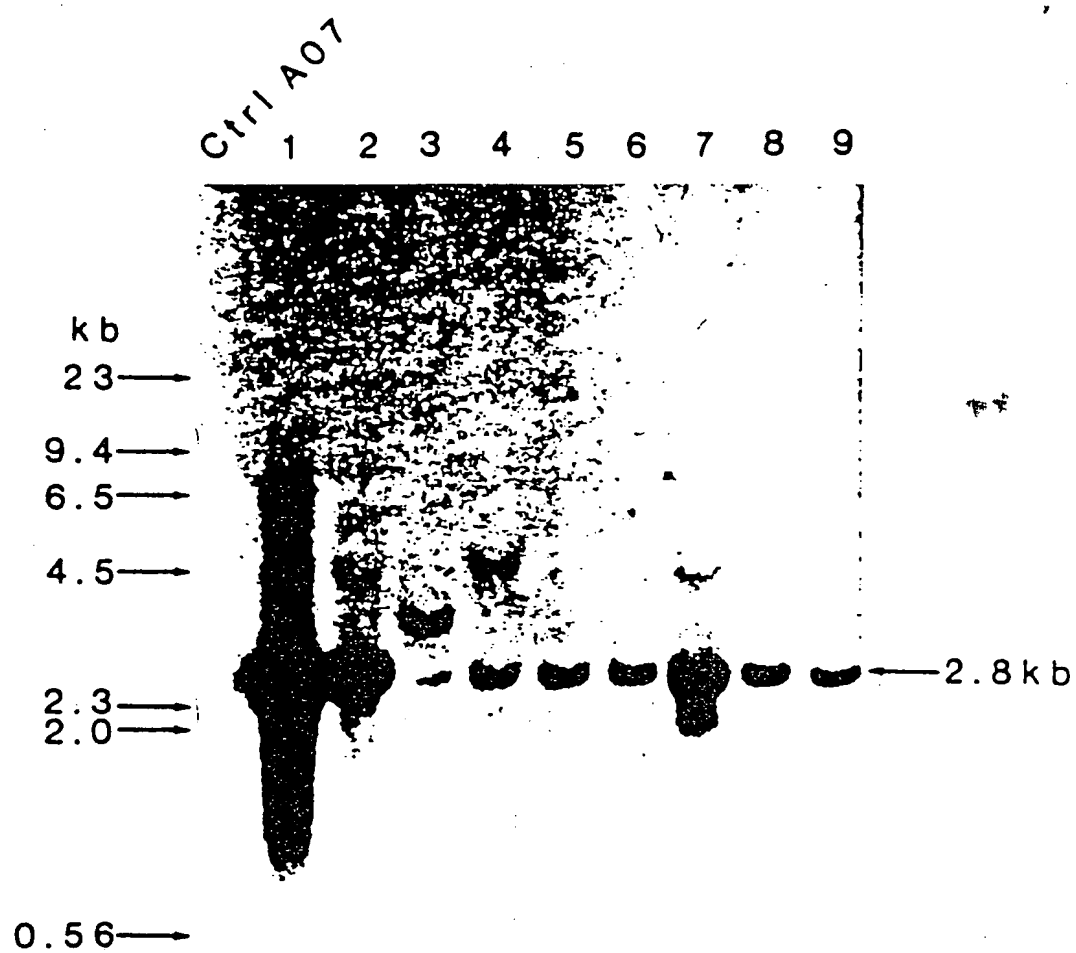


FIG.6

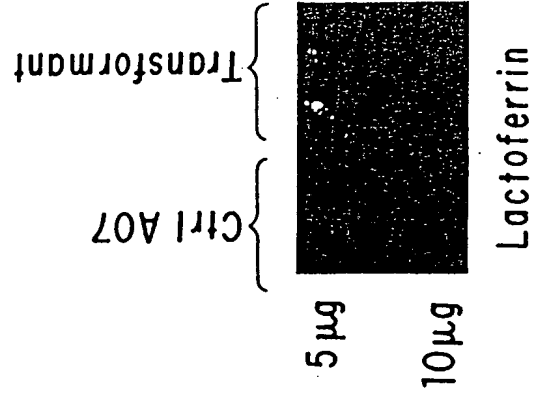
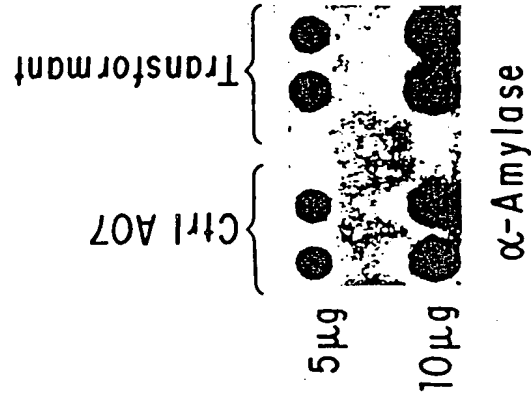
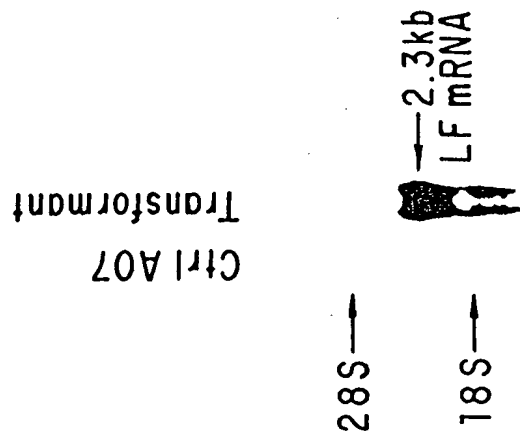


FIG.7A

FIG.7B

FIG.7C

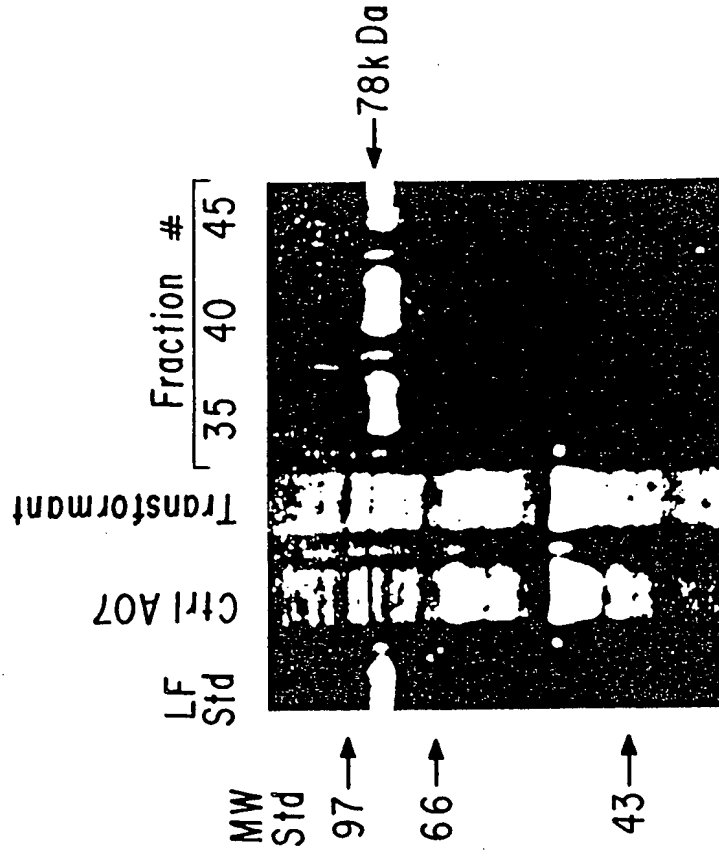


FIG.8B

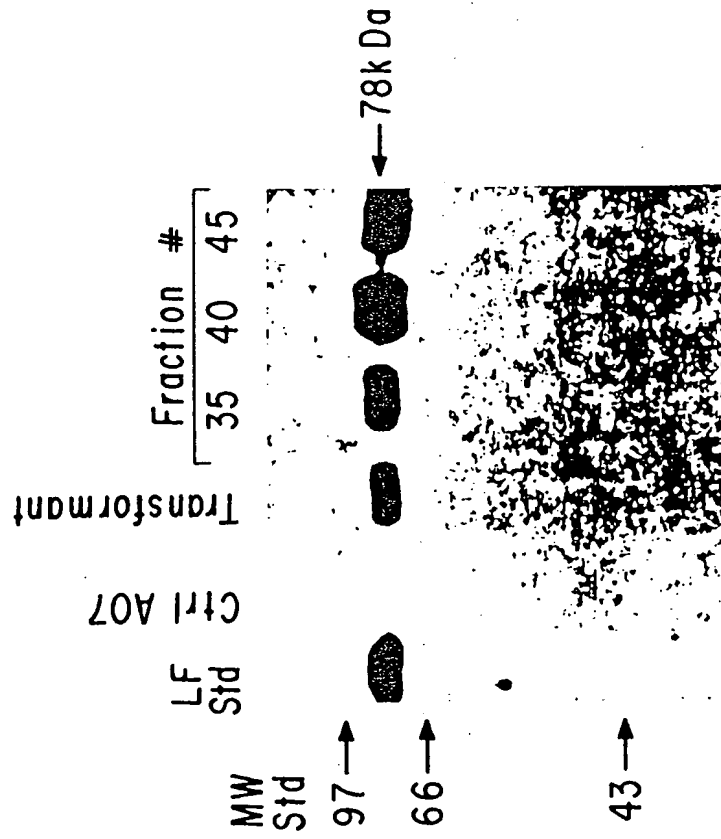


FIG.8A

α -Amlase Signal Sequence | Mature α -Amylase
 1) ————— AlaLeuAlaAlaThrProAlaAspTrpArgSerGlnSer

Lactoferrin Signal Sequence | Mature Human Lactoferrin
 2) ————— CysLeuAlaGlyArgArgArgArgSerValGlnTrpCys

α -Amylase Signal Sequence | Mature Recombinant Lactoferrin
 3) ————— AlaLeuAlaAlaGlyArgArgArgArgSerValGlnTrp*

FIG. 8C

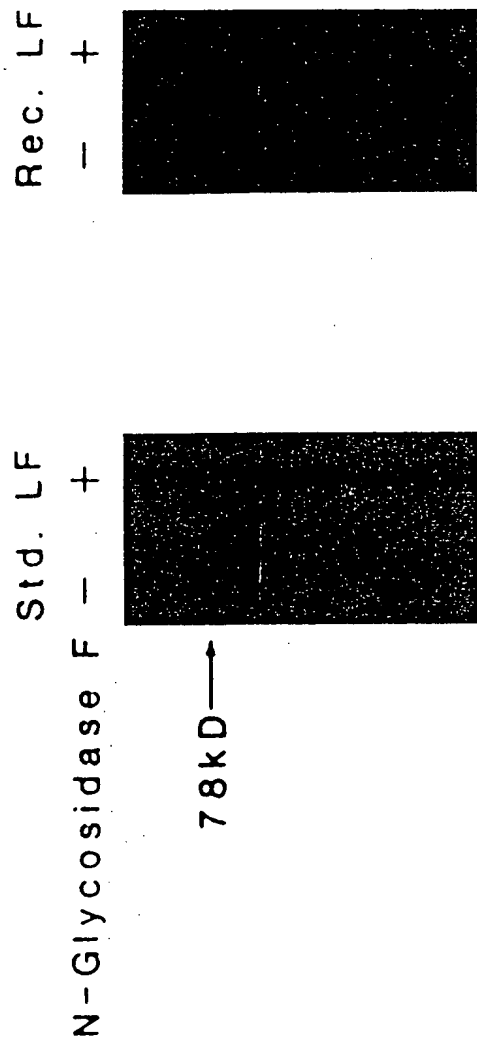


FIG.9A

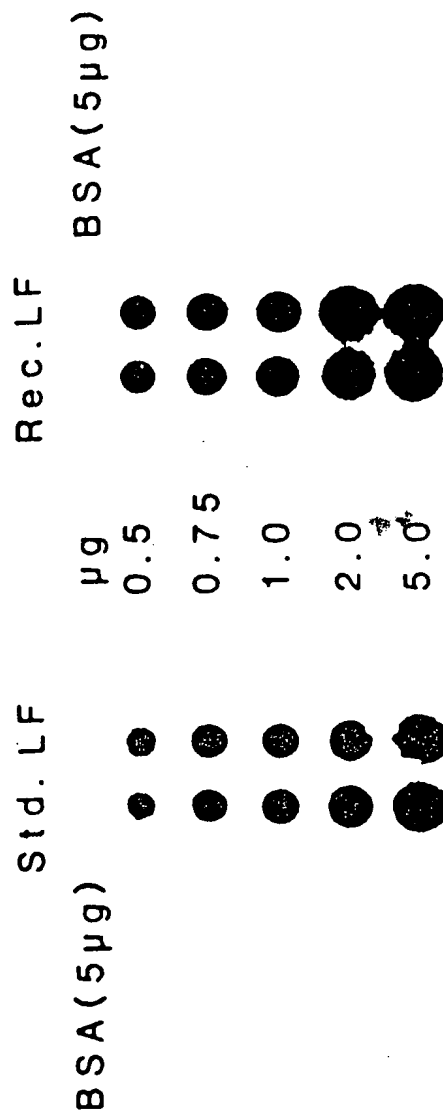


FIG.9B

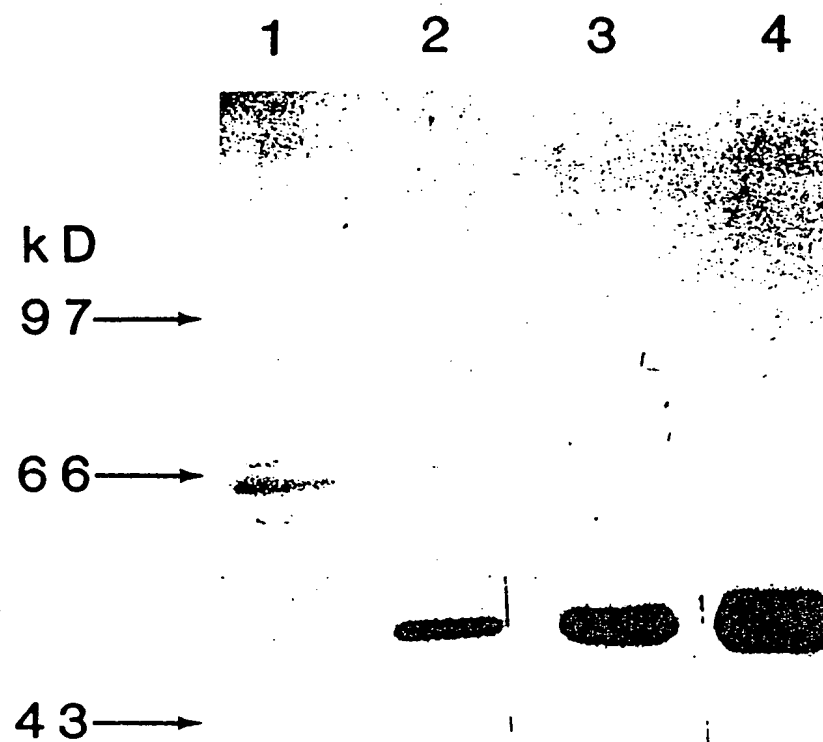


FIG.10

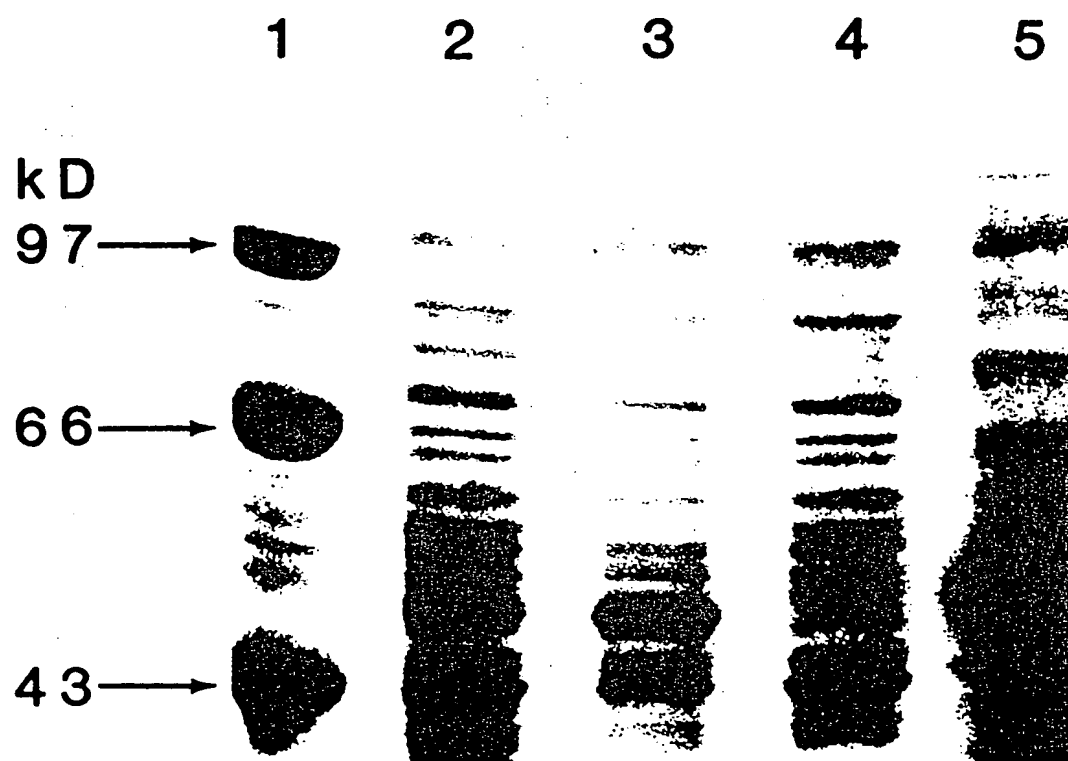


FIG.11

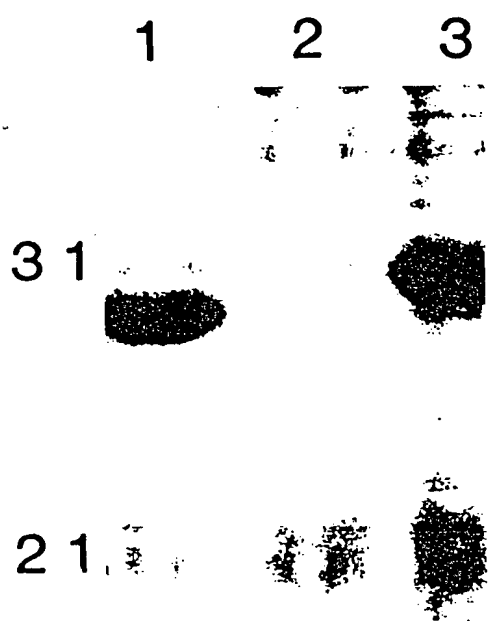


FIG.12A

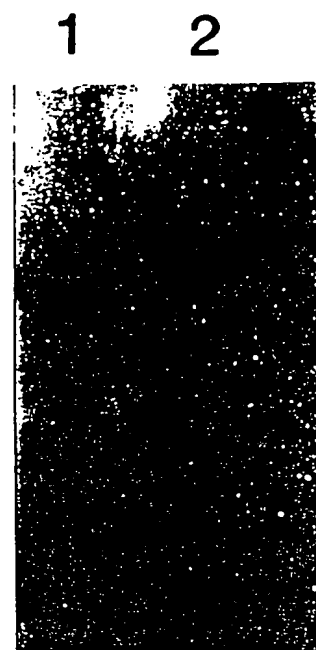


FIG.12B

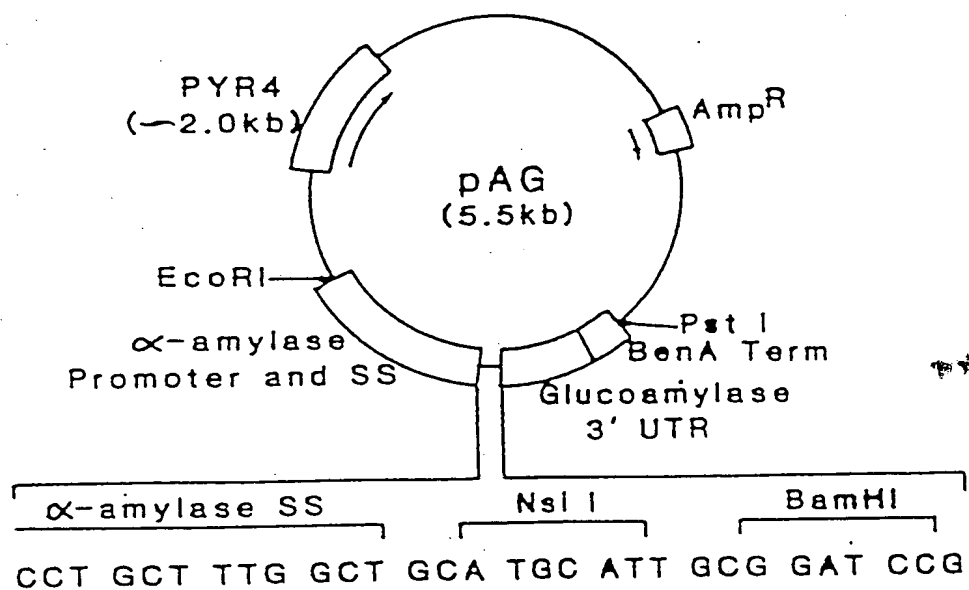


FIG. 13

1 NNNNGAGCCT TCGTTCGGGA GTCGCCCCAG GACGCCAGCC CATGAAGCTC
51 TTCGTCCCCG CCTCCTGTC CCTTGGAGCC CTTGGACTGT GTCTGGCTGC
101 CCCGAGGAAA AACGTTGAT GGTGTACCAT CTCCCAACCT GAGTGGTTCA
151 AATGCCGCAG ATGGCAGTGG AGGATGAAGA AGCTGGGTGC TCCCTCTATC
201 ACCTGTGTGA GCGGGGCCCTT TGCCTTGGAA TGTATTCCGG GCATCGCGGA
251 GAAAAAGGCG GATGCTGTGA CCCTGGATGG TGGCATGCTG TTTGAGGCGG
301 GCCGGGACCC CTACAACTG CGGCCAGTAG CAGCAGAGAT CTATGGGACC
351 AAAGAGTCTC CCCAAACCCA CTATTATGCT GTGGCCGTCT TGAAGAAGGG
401 CAGCAACTTT CAGCTGGACC AGCTGCAAGG CCGGAAGTCC TCCCATACGG
451 GCCTTGGCAG GTCCGCTGGG TGGATCATCC CTATGGGAAT CCTTCGCCCC
501 TACTTGAGCT GGACAGAGTC ACTCGAGCCC CTCCAGGGAG CTGTGGCTAA
551 ATTCTTCTCT GCCAGCTGTG TTCCCTGCAT TGATAGACAA CCATACCCCA
601 ACCTGTGTCA ACTGTGCAAG GGGGAGGGGG AGAACCAGTG TGCCTGCTCC
651 TCCCGGGAAC CATACTTCGG TTATTCTGCT GCCTTCAAGT GTCTGCAGGA
701 CGGGGCTGGA GACGTGSCCT TTGTTAAAGA GACGACAGTG TTTGAGAACT
751 TGCCAGAGAA GGCTGACAGG GACCAGTATG AGCTTCTCTG CCTGAACAAC
801 AGTCGGGCGC CAGTGGATGC GTTCAAGGAG TCCACCTGG CCCAGGTCCC
851 TTCTCATGCT GTCGTGGCCC GAAGTGTGGA TGGCAAGGAA GACTTGATCT
901 GGAAGCTTCT CAGCAAGGCG CAGGAGAAAT CTGGAAGAAA CAAGTCTCGG
951 AGCTTCCAGC TCTTTGGCTC TCCACCCGGC CAGAGGGACC TGCTGTTCAA
1001 AGACTCTGCT CTTGGGTTTT TGAGGATCCC CTCGAAGSTA GATTGGCCGC
1051 TGTACCTGGG CTCCCGCTAC TTGACCACCT TGAAGAACCT CAGGGAAACT
1101 GCGGAGGAGG TGAAGGCGCG GTACACCAGG STCGTGTGCT GTGCCGTGGG
1151 ACCTGAGGAG CAGAAGAAGT GCCAGCAGTG GAGCCAGCAG AGCGGCCAGA
1201 ACGTGACCTG TCCACGCGCG TCCACCACTG ACGACTGCAT CGTCCTGGTG
1251 CTGAAAGGGG AAGCAGATGC CCTGAACCTG GATCGAGGAT ATATCTACAC
1301 TCGGGGCAAG TGTGGCCTGG TGCCTGTCTT GGCAGAGAAC CGGAAATCCT
1351 CCAAACACAG TAGCCTAGAT TGTGTGCTGA GACCAACGGA AGGGTACCTT
1401 GCCGTGGCAG TTGTCAAGAA AGCAAATGAG GGGCTCACAT GGAATTCTCT

FIG. 14A

1451 GAAAGACAAG AAGTCGTGCC ACACCGCCGT GGACAGGACT GCAGGCTGGA
1501 ACATCCCCAT GGGCCTGATC GTCAACCAGA CAGGCTCCTG CGCATTTGAT
1551 GAATTCTTTA GTCAGAGCTG TGCCCCTGGG GCTGACCCGA AATCCAGACT
1601 CTGTGCCTTG TGTGCTGGCG ATGACCAGGG CCTGGACAAG TGTGTGCCCA
1651 ACTCTAAGGA GAAGTACTAT GGCTATACCG GGGCTTTCAG GTGCCTGGCT
1701 GAGGACGTTG GGGACGTTGC CTTTGTGAAA AACGACACAG TCTGGGAGAA
1751 CACGAATGGA GAGAGCACTG CAGACTGGGC TAAGAACTTG AATCGTGAGG
1801 ACTTCAGGTT GCTCTGCCTC GATGGCACCA GGAAGCCTGT GACGGAGGCT
1851 CAGAGCTGCC ACCTGGCGGT GGCCCCGAAT CACGCTGTGG TGTCTCGGAG
1901 CGATAGGGCA GCACACGTGA AACAGGTGCT GCTCCACCAG CAGGCTCTGT
1951 TTGGGAAAAA TGGAAAAAAC TGCCCGGACA AGTTTTGTTT GTTCAAATCT
2001 GAAACCAAAA ACCTTCTGTT CAATGACAAC ACTGAGTGTC TGGCCAAACT
2051 TGGAGGCAGA CCAACGTATG AAGAATATTT GGGGACAGAG TATGTCACGG
2101 CCATTGCCAA CCTGAAAAAA TGCTCAACCT CCCCCTTCT GGAAGCCTGC
2151 GCCTTCCTGA CGAGGTAAAG CCTGCAAAGA AGCTAGCCTG CCTCCCTGGG
2201 CCTCAGCTCC TCCCTGCTCT CAGCCCCAAT CTCCAGGCGC GAGGGACCTT
2251 CCTCTCCCTT CCTGAAGTCG GATTTTTGCC AAGCTCATCA GTATTTACAA
2301 TTCCCTGCTG TCATTTTAGC AAGAAATAAA ATTAGAAATG CTGTTGAAAA
2351 A

FIG. 14B

MKLFVPALLSLGALGLCLAAPRKNNRWCTISQPEWFKCRRWQWRMKKLGAPSIITCVRRAFAL
ECIPGIAEKKADAVTLDGGMVFEAGRDPYKLRPVAAEIYGTKE SPQTHYYAVAVVKKGSNFQ
LDQLQGRKSCHTGLGRSAGWII PMGILRPYLSWTESLEPLQGAVAKFFSASCVP CIDROAYP
NLCQLCKGEGENQCACSSREPYFGYSGAFKCLQDGAGDVA FVKETT VFENLPEKADRDQYEL
LCLNNSRAPVDAFKECHLAQVP SHAVVARSVDGKEDLIWKLLSKAQEKSGKNKSRSFQLFGS
PPGQRDLLFKDSALGFLRIPSKVDSALYLGSRYLTTLKNLRETAEV KARYTRVVWCAVGPE
EQKKCQQWSQQSGQNVTCATASTTDDCIVLVKGEADALNLDGGYIYTAGKCGLVPVLAENR
KSSKHSSLD CVLRPTEGYLAVAVVKKANEGLTWN SLKDKKSCHTAVDRTAGWNI PMGLIVNQ
TGSCAFDEFFSQSCAPGADPKSRLCALCAGDDQGLDKCVPNSKEKY YGYTGAFRCLAEDVGD
VAFVKNDTVWENTNGESTADWAKNLNREDFRLCLDGTRKPVTEAQ SCHLAVAPNHAVVSRS
DRAAHVKQVLLHQALFGKNGKNCPDKFCLFKSETKNLLFNDNTECLAKLGGRPTYE EYLG
EYVTAIANLKKCSTSPLEACAFLTR

FIG. 14C

1 ACATGAAGCT CTTTCATCCCC GCCCTGCTGT TCCTCGGGAC ACTTGGACTG
51 TGTCTGGCTG CCCCTAAGAA AGGGGTTCGA TGGTGTGTCA TATCCACAGC
101 AGAGTATTCA AAATGCCGCC AGTGGCAATC AAAGATAAGA AGAACTAATC
151 CCATGTTCTG CATAAGGAGG GCTTCTCCCA CTGACTGTAT CCGGGCCATC
201 GCGGCAAAAA GGGCAGATGC TGTGACCCTT GATGGTGGTT TGGTGTTTGA
251 AGCAGACCAG TACAACTGC GGCCGGTAGC AGCGGAGATC TACGGGACAG
301 AAGAGAATCC CCAAACCTAC TATTATGCTG TGGCTGTAGT GAAGAAAGGT
331 TTCAACTTTC AGAACCAGCT ACAAGGTGGA AAGTCCTGCC ACACAGGCCCT
401 TGGCAGGTCT GCGGGGTGGA ATATCCCTAT AGGGTTACTT CCGCGTTCT
451 TGGACTGGGC AGGGCCACCT GAGCCCTCC AGAAAGCTGT GSCCAAATTC
501 TTCTCTCAGA GCTGTGTGCC CTGCGCAGAT GGAATGCGT ATCCCAACCT
551 GTGTCAGCTG TGCATAGGGA AAGSGAAGA TAAATGTGCT TGTTCCTCCC
601 AGGAACCGTA TTTTGGCTAT TCCGCTGCCT TCAACTGTCT GCACAAAGGG
651 ATTGGAGATG TGGCTTTTGT CAAGGAGAGT ACACTGTTTG AGAACCTGCC
701 ACAGAAGGCT GACCGGGACA AATACGAGCT ACTCTGCCCC GACAATACTC
751 GAAAGCCAGT GGAAGCATTG AGGGAGTGGC ACCTTGCCCC GGTCCCTTCT
801 CATGCTGTTG TGGCCCGAAG TGTGAATGGC AAGGAGAACT CCATCTGGGA
851 GCTTCTCTAC CAGTCACAGA AAAAGTTTGG AAAAAGCAAT CCACAGGAGT
901 TCCAGCTCTT TGGCTCTCCT GGTGAGCAGA AGGACCTCCT GTTTAGAGAT
951 GCTACCATCG GTTTTTTTGA GATCCCCCTCA AAGATAGATT CTAAGCTGTA
1001 CCTGGGCCCTC CCGTACCTTA CTGCCATCCA GGGCCTGAGG GAAACGGCAG
1051 CGGAGGTGGA GCGCGGGCAG GCGAAGSTCG TGTGGTGGC CGTGGGTCCA
1101 GAGGAGCTGC GCAAGTGCCG GCACTGGAGC AGCCAGAGCA GCCAGAACCT
1151 GAACTGCAGC CTGGCCTCCA CCACCGAGGA CTGCATCGTC CAGGTGCTGA
1201 AAGGAGAAGC TGATGCTATG AGCTTGGATG GAGGATTTAT CTACACTGCC
1251 GGCAAGTGTG GTTTGGTGGC TGTCTGGCA GAGAACCAA AATCTGCCCA
1301 AAGCAGTAGC TCAGACTGTG TGCATAGACC AACACAAGGG TATTTTGGCG
1351 TGGCGGTTGT CAGGAAAGCA AATGGTGGTA TCACCTGGAA CTCTGTGAGA
1401 GGCACGAAGT CCTGCCACAC TGCTGTGGAC AGGACAGCAG GCTGGAACT

FIG. 15A

1451 CCCCATGGGC CTGCTTGTCA ACCAGACAGG CTCCTGCAAA TTTGACGAAT
1501 TCTTTAGTCA AAGCTGTGCT CCTGGGTCTC AGCCGGGATC CAATCTCTGT
1551 GCACTGTGTG TTGGCAATGA CCAGGGCGTG GACAAGTGTG TGCCCAACAG
1601 TAATGAGAGA TACTATGGTT ACACCGGGGC TTTCAGGTGC CTGGCTGAGA
1651 ATGCTGGGGA TGTGGCGTTT GTGAAAGATG TCACTGTCTT GGACARCACC
1701 AATGGACAGA ACACAGAAGA GTGGGCCAGG GAATTGAGGT CAGATGACTT
1751 TGAGCTGCTG TGCCTTGATG GCACCAGGAA GCCTGTGACT GAGGCTCAGA
1801 ACTGTCACCT GGCTGTGGCC CCCAGTCATG CTGTGCTCTC TCGGAAGGAA
1851 AAGGCAGCAC AGGTGGAACA GGTGCTACTC ACTGAGCAGG CTCAGTTTGG
1901 AAGATACGGA AAAGACTGCC CGGACAAGTT TTGCTTGTTT CGGTCTGAGA
1951 CCAAAAACCT TCTGTTCAAC GACAACACGG AGGTTCTGGC CCAACTCCAA
2001 GGCAAAACAA CATACGAAAA ATATTTGGGA TCAGASTATG TCACAGCCAT
2051 CGCTAACCTG AAACAGTGCT CAGTCTCCCC GCTTCTGGAA GCCTGTGCCT
2101 TCATGATGAG GTAAAACCGG AAAAGAAGCT GCCCGCCTCC CCAGGGGCCT
2151 CAGCTTTCCC TCCTCCCGTC TTGATTCCCA GCTGCCCTGG GCCTGCCTCT
2201 CTCCCTTCCT GAGGGCAGAC TTTGTTCAAC TCATCCGTTT TCACAATTCC
2251 CTCGTGCCG

FIG. 15B

1

2

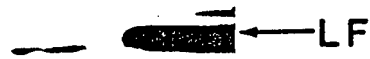


FIG.16

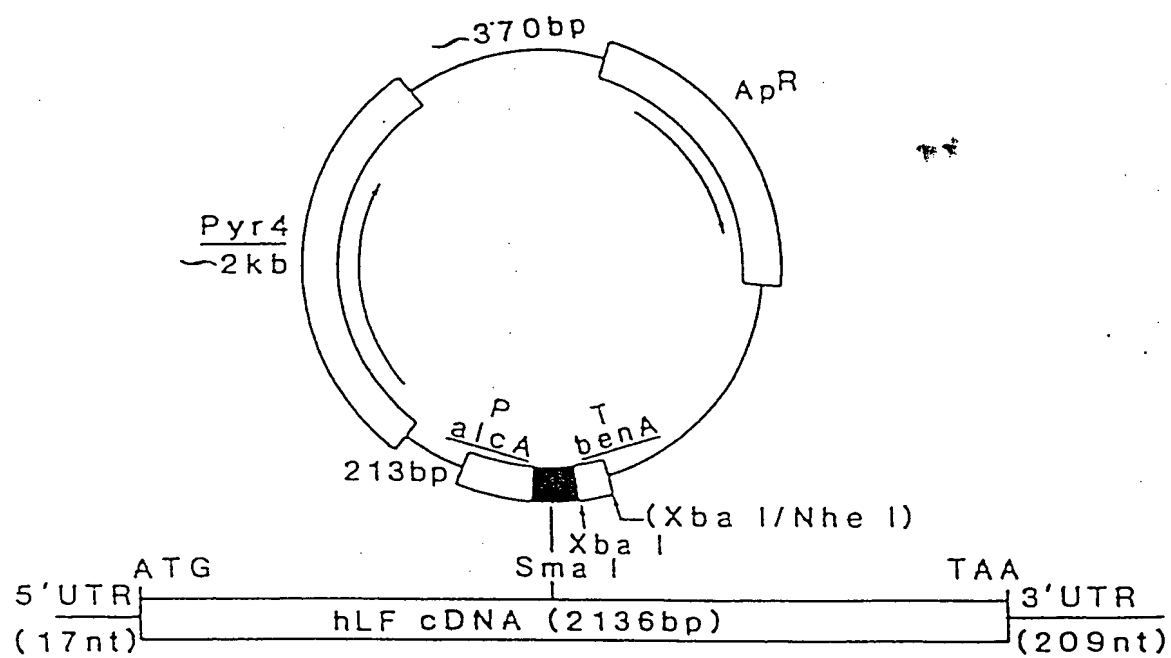


FIG. 17

(Linear) MAPSORT of: hlf2 check: 7473 from: 1 to: 2360
Mismatch: 0 MinCuts = 1 MaxCuts: 10

AccI GT'mk_AC

Cuts at: 0 319 2360

Size: 319 2041

AceIII CAGCTCnnnnnnnn'nnnn

Cuts at: 0 948 1125 2183 2219 2360

Size: 948 177 1058 36 141

Fragments arranged by size:

1058 948 177 141 36

AhdI GACnn_n'nnGTC

Cuts at: 0 472 2360

Size: 472 1888

AlwI GGATCnnnn'n

Cuts at: 0 1341 1955 2360

Size: 1341 614 405

Fragments arranged by size:

1341 614 405

AlwNI CAG_nnn'CTG

Cuts at: 0 1139 1913 2360

Size: 1139 774 447

Fragments arranged by size:

1139 774 447

ApaI G_GGCC'C

Cuts at: 0 56 2360

Size: 56 2304

ApaBI GCA_nnnnn'TGC

Cuts at: 0 1140 1789 2360

Size: 1140 649 571

Fragments arranged by size:

1140 649 571

ApaLI G'TGCA_C

Cuts at: 0 101 2360

Size: 101 2259

ApoI r'AATT_y

Cuts at: 0 1 930 1527 1932 2136 2318 2360

Size: 1 929 597 405 204 182 42

Fragments arranged by size:

929 597 405 204 182 42 1

FIG. 18A

AvaI C'yCGr_G
Cuts at: 0 48 117 820 1010 1571 2360
Size: 48 69 703 190 561 789
Fragments arranged by size:
789 703 561 190 69 48

AvaII G'GwC_C
Cuts at: 0 325 439 495 725 824 2067 2360
Size: 325 114 56 230 99 1243 293
Fragments arranged by size:
1243 325 293 230 114 99 56

BanI G'GyrC_C
Cuts at: 0 657 1004 1298 1675 2360
Size: 657 347 294 377 685
Fragments arranged by size:
685 657 377 347 294

BanII G_rGCy'C
Cuts at: 0 56 508 1521 2360
Size: 56 452 1013 839
Fragments arranged by size:
1013 839 452 56

BbsI GAAGACnn'nnnn_
Cuts at: 0 20 2360
Size: 20 2340

BbvI GCAGCnnnnnnnn'nnnn_
Cuts at: 0 168 394 528 1079 1126 1189 1780 1827
Size: 168 226 134 551 47 63 591 47
Cuts at: 1827 1900 2360
Size: 73 460
Fragments arranged by size:
591 551 460 226 168 134 73 63 47 47

Bce83I CTTGAGnnnnnnnnnnnnnn'_nn'
Cuts at: 0 1088 1187 2360
Size: 1088 99 1173
Fragments arranged by size:
1173 1088 99

BceII ACGGCnnnnnnnnnnnn'_n_
Cuts at: 0 62 343 823 1447 1670 1855 2360
Size: 62 281 480 624 223 185 505
Fragments arranged by size:
624 505 480 281 223 185 62

FIG. 18B

BfaI C'TA_G
 Cuts at: 0 952 1414 1834 2360
 Size: 952 462 420 526
 Fragments arranged by size:
 952 526 462 420

BfiI ACTGGG
 Cuts at: 0 1664 2360
 Size: 1664 696

BglI GCCn_nnn'nGGC
 Cuts at: 0 427 843 1807 2360
 Size: 427 416 964 553
 Fragments arranged by size:
 964 553 427 416

BglII A'GATC_T
 Cuts at: 0 965 1575 2360
 Size: 965 610 785
 Fragments arranged by size:
 965 785 610

BmgI GkGCCC
 Cuts at: 0 54 1007 1557 1631 2360
 Size: 54 953 550 74 729
 Fragments arranged by size:
 953 729 550 74 54

BpmI CTGGAGnnnnnnnnnnnnnnn_nn'
 Cuts at: 0 706 1714 2360
 Size: 706 1008 646
 Fragments arranged by size:
 1008 706 646

Bpu10I CC'TnA_GC
 Cuts at: 0 502 1765 2188 2360
 Size: 502 1263 423 172
 Fragments arranged by size:
 1263 502 423 172

BsaWI w'CCGG_w
 Cuts at: 0 1672 2360
 Size: 1672 688

BsaXI ACnnnnnCTCC
 Cuts at: 0 87 1037 1268 2360
 Size: 87 950 231 1092
 Fragments arranged by size:
 1092 950 231 87

FIG. 18C

BsbI CAACAC
 Cuts at: 0 778 2014 2227 2360
 Size: 778 1236 213 133
 Fragments arranged by size:
 1236 778 213 133

BscGI CCCGT
 Cuts at: 0 324 494 681 1517 2360
 Size: 324 170 187 836 843
 Fragments arranged by size:
 843 836 324 187 170

BseRI GAGGAGnnnnnnnnn_nn'
 Cuts at: 0 617 1095 1181 2360
 Size: 617 478 86 1179
 Fragments arranged by size:
 1179 617 478 86

BsgI GTGCAGnnnnnnnnnnnnnnn_nn'
 Cuts at: 0 577 2360
 Size: 577 1783

BsiEI CG_ry'CG
 Cuts at: 0 10 2360
 Size: 10 2350

BsiHKA I G_wGCw'C
 Cuts at: 0 105 714 1592 2109 2360
 Size: 105 609 878 517 251
 Fragments arranged by size:
 878 609 517 251 105

BsmI GAATG_Cn'
 Cuts at: 0 1694 2360
 Size: 1694 666

BsmAI GTCTCn'nnnn_
 Cuts at: 0 187 670 682 1690 1882 2360
 Size: 187 483 12 1008 192 478
 Fragments arranged by size:
 1008 483 478 192 187 12

BsmBI CGTCTCn'nnnn_
 Cuts at: 0 670 682 1690 2360
 Size: 670 12 1008 670
 Fragments arranged by size:
 1008 670 670 12

BsmFI GGGACnnnnnnnnnn'nnnn_
 Cuts at: 0 338 479 614 762 810 2080 2360
 Size: 338 141 135 148 48 1270 280
 Fragments arranged by size:
 1270 338 280 148 141 135 48

FIG. 18D

Bsp24I GACnnnnnnTGGnnnnnnnnnnnn'

Cuts at: 0 52 84 239 271 569 601 2062 2094

Size: 52 32 155 32 298 32 1461 32

Cuts at: 2094 2360

Size: 266

Fragments arranged by size:

1461 298 266 155 52 32 32 32 32

Bsp1286I G_dGCh'C

Cuts at: 0 56 105 508 714 1009 1521 1559 1592

Size: 56 49 403 206 295 512 38 33

Cuts at: 1592 1633 2109 2360

Size: 41 476 251

Fragments arranged by size:

512 476 403 295 251 206 56 49 41 38 33

BspMI ACCTGCnnnn'nnnn

Cuts at: 0 1194 2360

Size: 1194 1166

BsrI ACTG_Gn'

Cuts at: 0 206 789 1154 1667 1979 2360

Size: 206 583 365 513 312 381

Fragments arranged by size:

583 513 381 365 312 206

BsrDI GCAATG_nn'

Cuts at: 0 220 1646 2360

Size: 220 1426 714

Fragments arranged by size:

1426 714 220

BsrGI T'GTAC_A

Cuts at: 0 1273 2360

Size: 1273 1087

BstXI CCAn_nnnn'nTGG

Cuts at: 0 942 1161 1256 2360

Size: 942 219 95 1104

Fragments arranged by size:

1104 942 219 95

BstYI r'GATC_y

Cuts at: 0 965 1575 1947 2360

Size: 965 610 372 413

Fragments arranged by size:

965 610 413 372

FIG. 18E

Bsu36I CC'TnA_GG

Cuts at: 0 2142 2360

Size: 2142 218

CjeI ACnnnnnnTGGnnnnnn'nnnnnn_

Cuts at: 0 79 188 266 563 618 2056 2360

Size: 79 109 78 297 55 1438 304

Fragments arranged by size:

1438 304 297 109 79 78 55

CviRI TG'CA

Cuts at: 0 103 184 404 558 1216 1281 1476 1525

Size: 103 81 220 154 658 65 195 49

Cuts at: 1525 1704 1730 2360

Size: 179 26 630

Fragments arranged by size:

658 630 220 195 179 154 103 81
65 49 26

DdeI C'TnA_G

Cuts at: 0 502 536 672 1684 1765 1828 2017 2142

Size: 502 34 136 1012 81 63 189 125

Cuts at: 2142 2188 2297 2360

Size: 46 109 63

Fragments arranged by size:

1012 502 189 136 125 109 81 63 63 46 34

DpnI GA'TC

Cuts at: 0 967 1348 1406 1577 1949 2360

Size: 967 381 58 171 372 411

Fragments arranged by size:

967 411 381 372 171 58

DraIII CAC_nnn'GTG

Cuts at: 0 852 2020 2360

Size: 852 1168 340

Fragments arranged by size:

1168 852 340

DsaI C'CryG_G

Cuts at: 0 358 1462 1492 1852 1870 2036 2360

Size: 358 1104 30 360 18 166 324

Fragments arranged by size:

1104 360 358 324 166 30 18

EaeI y'GGCC_r

Cuts at: 0 74 523 2026 2360

Size: 74 449 1503 334

Fragments arranged by size:

1503 449 334 74

FIG. 18F

```

Earl CTCTTCn'nnn_
Cuts at: 0 152 1509 2216 2360
Size: 152 1357 707 144
Fragments arranged by size:
1357 707 152 144
EciI TCCGCC
Cuts at: 0 313 891 2360
Size: 313 578 1469
Fragments arranged by size:
1469 578 313
Eco57I CTGAAGnnnnnnnnnnnnnnnn nn'
Cuts at: 0 432 629 2269 2360
Size: 432 197 1640 91
Fragments arranged by size:
1640 432 197 91
EcoNI CCTnn'n_nnAGG
Cuts at: 0 1372 1905 2248 2360
Size: 1372 533 343 112
Fragments arranged by size:
1372 533 343 112
EcoOI109I rG'GnC_Cy
Cuts at: 0 52 53 725 824 2231 2360
Size: 52 1 672 99 1407 129
Fragments arranged by size:
1407 672 129 99 52 1
EcoRI G'AATT_C
Cuts at: 0 1 2136 2360
Size: 1 2135 224
Fragments arranged by size:
2135 224 1
EcoRV GAT'ATC
Cuts at: 0 1380 2360
Size: 1380 980
FauI CCCGCnnnn'nn_
Cuts at: 0 590 1099 2360
Size: 590 509 1261
Fragments arranged by size:
1261 590 509
FokI GGATGnnnnnnnnnn'nnnn_
Cuts at: 0 189 460 882 1044 1272 1895 2252 2360
Size: 189 271 422 162 228 623 357 108
Fragments arranged by size:
623 422 357 271 228 189 162 108

```

FIG. 18G

FspI TGC'GCA
 Cuts at: 0 1143 2360
 Size: 1143 1217
 GdiII y'GGCC_G
 Cuts at: 0 74 2360
 Size: 74 2286
 HaeI wGG'CCw
 Cuts at: 0 123 219 280 430 525 2028 2360
 Size: 123 96 61 150 95 1503 332
 Fragments arranged by size:
 1503 332 150 123 96 95 61
 HgiEI ACCnnnnnnGGT
 Cuts at: 0 254 2360
 Size: 254 2106
 HhaI G_CG'C
 Cuts at: 0 1106 1144 1793 2360
 Size: 1106 38 649 567
 Fragments arranged by size:
 1106 649 567 38
 Hin4I GAbnnnnnvTC
 Cuts at: 0 471 727 1573 1578 1580 2263 2360
 Size: 471 256 846 5 2 683 97
 Fragments arranged by size:
 846 683 471 256 97 5 2
 HinfI G'AnT_C
 Cuts at: 0 195 881 981 1020 1862 2032 2360
 Size: 195 686 100 39 842 170 328
 Fragments arranged by size:
 842 686 328 195 170 100 39
 HphI GGTGAnnnnnnn_n'
 Cuts at: 0 380 916 1626 2360
 Size: 380 536 710 734
 Fragments arranged by size:
 734 710 536 380
 MaeII A'CG_T
 Cuts at: 0 691 1699 2360
 Size: 691 1008 661
 Fragments arranged by size:
 1008 691 661

FIG. 18H

MaeIII 'GTnAC_
 Cuts at: 0 245 760 922 1149 1181 1338 1718 1823
 Size: 245 515 162 227 32 157 380 105
 Cuts at: 1823 2360
 Size: 537
 Fragments arranged by size:
 537 515 380 245 227 162 157 105 32
 MboII GAAGAnnnnnnnn_n'
 Cuts at: 0 20 169 383 524 876 1496 2170 2173
 Size: 20 149 214 141 352 620 674 3
 Cuts at: 2173 2203 2360
 Size: 30 157
 Fragments arranged by size:
 674 620 352 214 157 149 141 30 20 3
 MmeI TCCrACnnnnnnnnnnnnnnnnnnnn_nn'
 Cuts at: 0 30 2360
 Size: 30 2330
 MscI TGG'CCA
 Cuts at: 0 525 2028 2360
 Size: 525 1503 332
 Fragments arranged by size:
 1503 525 332
 MslI CAynn'nnrTG
 Cuts at: 0 352 1461 2360
 Size: 352 1109 899
 Fragments arranged by size:
 1109 899 352
 MspI C'CG_G
 Cuts at: 0 553 821 1042 1097 1673 1959 2360
 Size: 553 268 221 55 576 286 401
 Fragments arranged by size:
 576 553 401 286 268 221 55
 MspAII CmG'CkG
 Cuts at: 0 181 392 444 519 544 2360
 Size: 181 211 52 75 25 1816
 Fragments arranged by size:
 1816 211 181 75 52 25
 NciI CC's_GG
 Cuts at: 0 553 821 822 1097 1959 2360
 Size: 553 268 1 275 862 401
 Fragments arranged by size:
 862 553 401 275 268 1

FIG. 18I

NcoI C'CATG_G
 Cuts at: 0 1492 1852 2036 2360
 Size: 1492 360 184 324
 Fragments arranged by size:
 1492 360 324 184

NdeI CA'TA_TG
 Cuts at: 0 2051 2360
 Size: 2051 309

NlaIII _CATG'
 Cuts at: 0 20 837 1253 1496 1762 1856 1869 2040
 Size: 20 817 416 243 266 94 13 171
 Cuts at: 2040 2360
 Size: 320
 Fragments arranged by size:
 817 416 320 266 243 171 94 20 13

PstI GAGTCnnnn'n_
 Cuts at: 0 189 975 2026 2360
 Size: 189 786 1051 334
 Fragments arranged by size:
 1051 786 334 189

Psp5II rG'GwC_Cy
 Cuts at: 0 725 824 2360
 Size: 725 99 1536
 Fragments arranged by size:
 1536 725 99

PstI C_TGCA'G
 Cuts at: 0 1283 1478 2360
 Size: 1283 195 882
 Fragments arranged by size:
 1283 882 195

PvuII CAG'CTG
 Cuts at: 0 181 392 519 544 2360
 Size: 181 211 127 25 1816
 Fragments arranged by size:
 1816 211 181 127 25

RsaI GT'AC
 Cuts at: 0 642 1032 1275 2360
 Size: 642 390 243 1085
 Fragments arranged by size:
 1085 642 390 243

FIG. 18J

SanDI GG'GwC_CC
 Cuts at: 0 824 2360
 Size: 824 1536
 SapI GCTCTTCn'nnn_
 Cuts at: 0 1509 2216 2360
 Size: 1509 707 144
 Fragments arranged by size:
 1509 707 144
 Sau3AI 'GATC_
 Cuts at: 0 965 1346 1404 1575 1947 2360
 Size: 965 381 58 171 372 413
 Fragments arranged by size:
 965 413 381 372 171 58
 SfaNI GCATCnnnnn'nnnn_
 Cuts at: 0 230 860 1225 1235 2360
 Size: 230 630 365 10 1125
 Fragments arranged by size:
 1125 630 365 230 10
 SfcI C'TryA_G
 Cuts at: 0 304 460 1279 1474 2360
 Size: 304 156 819 195 886
 Fragments arranged by size:
 886 819 304 195 156
 SmaI CCC'GGG
 Cuts at: 0 822 2360
 Size: 822 1538
 Sse8647I AG'GwC_CT
 Cuts at: 0 725 2360
 Size: 725 1635
 SspI AAT'ATT
 Cuts at: 0 1539 2061 2360
 Size: 1539 522 299
 Fragments arranged by size:
 1539 522 299
 SnuI AGG'CCT
 Cuts at: 0 280 430 2360
 Size: 280 150 1930
 Fragments arranged by size:
 1930 280 150
 StyI C'CwwG_G
 Cuts at: 0 1034 1492 1852 2036 2234 2360
 Size: 1034 458 360 184 198 126
 Fragments arranged by size:
 1034 458 360 198 184 126

FIG. 18K

TaqI T'CG_A
 Cuts at: 0 999 1804 2360
 Size: 999 805 556
 Fragments arranged by size:
 999 805 556

TaqII GACCGAnnnnnnnnn_nn'
 Cuts at: 0 342 2360
 Size: 342 2018

TauI GCsGC
 Cuts at: 0 310 380 2360
 Size: 310 70 1980
 Fragments arranged by size:
 1980 310 70

TfiI G'AwT_C
 Cuts at: 0 881 1020 1862 2360
 Size: 881 139 842 498
 Fragments arranged by size:
 881 842 498 139

ThaI CG'CG
 Cuts at: 0 1106 2360
 Size: 1106 1254

TseI GCwGC
 Cuts at: 0 182 383 517 1093 1140 1178 1794 1841
 Size: 182 201 134 576 47 38 616 47
 Cuts at: 1841 1914 2360
 Size: 73 446
 Fragments arranged by size:
 616 576 446 201 182 134 73 47 38

Tsp45I 'GTsAC_
 Cuts at: 0 245 922 1181 1338 1718 1823 2360
 Size: 245 677 259 157 380 105 537
 Fragments arranged by size:
 677 537 380 259 245 157 105

Tsp509I 'AATT_
 Cuts at: 0 1 485 930 1527 1932 2136 2280 2318
 Size: 1 484 445 597 405 204 144 38
 Cuts at: 2318 2360
 Size: 42
 Fragments arranged by size:
 597 484 445 405 204 144 42 38

FIG. 18L

Tth111I GACn'n_nGTC
 Cuts at: 0 64 2360
 Size: 64 2296
 Tth111II CAArCAnnnnnnnnnn_nn'
 Cuts at: 0 708 2360
 Size: 708 1652
 UbaCI wGTACw
 Cuts at: 0 1275 2360
 Size: 1275 1085
 XcmI CCAnnnn_n'nnnnTGG
 Cuts at: 0 484 2360
 Size: 484 1876

Enzymes that do cut and were not excluded:

AccI	AceIII	AhdI	AlwI	AlwNI
ApaI	ApaBI	ApaLI	ApoI	AvaI
AvaII	BanI	BanII	BbsI	BbvI
Bce83I	BceFI	BfaI	BfiI	BglI
BglII	BmgI	BpmI	Bpu10I	BsaWI
BsaXI	BsbI	BscGI	BseRI	BsgI
BsiEI	BsiHKA I	BsmI	BsmAI	BsmBI
BsmFI	Bsp24I	Bsp1286I	BspMI	BsrI
BsrDI	BsrGI	BstXI	BstYI	Bsu36I
CjeI	CviRI	DdeI	DpnI	DraIII
DsaI	EaeI	EarI	EciI	Eco57I
EcoNI	EcoO109I	EcoRI	EcoRV	FauI
FokI	FspI	GdiII	HaeI	HgiEII
HhaI	Hin4I	HinfI	HphI	MaeII
MaeIII	MboII	MmeI	MscI	MslI
MspI	MspA1I	NciI	NcoI	NdeI
NlaIII	PleI	Psp5II	PstI	PvuII
RsaI	SanDI	SapI	Sau3AI	SfaNI
SfcI	SmaI	Sse8647I	SspI	StuI
StyI	TaqI	TaqII	TauI	TfiI
ThaI	TseI	Tsp45I	Tsp509I	Tth111I
Tth111II	UbaCIXcmI			

Enzymes that do not cut:

AatII	AflII	AflIII	AscI	AvrII
BaeI	BamHI	BcgI	BcgI	BclI
BpII	Bpu1102I	BsaI	BsaAI	BsaBI
BsaHI	BspEI	BspGI	BspLU11I	BsrBI
BsrFI	BssHII	BssSI	Bst1107I	BstEII
Clal	DraI	DrdI	DrdII	EagI
Eco47III	FseI	HaeII	HgaI	HincII

FIG. 18M

HindIII	HpaI	KpnI	MluI	MseI
MunI	NarI	NgoAIV	NheI	NotI
NruI	NsiI	NspI	NspV	PacI
Pfl1108I	PflMI	PinAI	PmeI	PmlI
PshAI	Psp1406I	PvuI	RcaI	RleAI
RsrII	SacI	SacII	SalI	ScaI
SexAI	SfiI	SgfI	SgrAI	SnaBI
SpeI	SphI	SrfI	Sse8387I	SunI
SwaI	VspI	XbaI	XhoI	XmnI

Enzymes excluded; MinCuts: 1

MaxCuts: 10

AciI	AluI	BccI	BsaJI	BsII
BsoFI	Cac8I	CjeI	CjePI	CjePI
CviJI	EcoRII	HaeIII	MnlI	MwoI
NlaIV	Sau96I	ScrFI	TspRI	

FIG. 18N

(Linear)MAPSORT of: piglac.gb_om check: 9514 from:1 to :2259
 LOCUS PIGLAC 2259 bp ss-mRNA MAM
 DEFINITION Sus scrofa lactoferrin mRNA, complete cds.
 ACCESSION M81327 M61828
 KEYWORDS lactoferrin.
 SOURCE Sus scrofa lactational mammary gland cDNA to mRNA.
 ORGANISM Sus scrofa . . .
 Mismatch: 0 MinCuts = 1 MaxCuts: 10
 With 209 enzymes: *

AceIII CAGCTCnnnnnnn'nnnn_
 Cuts at: 0 497 915 1092 1740 2239 2259
 Size: 497 418 177 648 499 20

Fragments arranged by size:
 648 499 497 418 177 20

AlwI GGATCnnnn'n_
 Cuts at: 0 965 1531 1544 2036 2259
 Size: 965 566 13 492 223

Fragments arranged by size:
 965 566 492 223 13

AlwNI CAG_nnn'CTG
 Cuts at: 0 219 1034 1148 1196 2259
 Size: 219 815 114 48 1063

Fragments arranged by size:
 1063 815 219 114 48

ApaLI G'TGCA_C
 Cuts at: 0 1549 2259
 Size: 1549 710

ApoI r'AATT_y
 Cuts at: 0 495 1488 1497 2259
 Size: 495 993 9 762

Fragments arranged by size:
 993 762 495 9

AvaI C'yCGr_G
 Cuts at: 0 33 787 2259
 Size: 33 754 1472

Fragments arranged by size:
 1472 754 33

AvaII G'GwC_C
 Cuts at: 0 791 932 1095 2259
 Size: 791 141 163 1164

Fragments arranged by size:
 1164 791 163 141

FIG. 19A

BaeI ACnnnnGTAYC

Cuts at: 0 1614 2259

Size: 1614 645

BamHI G'GATC_C

Cuts at: 0 1536 2259

Size: 1536 723

BanI G'GyrC_C

Cuts at: 0 624 1265 1636 1770 2259

Size: 624 641 371 134 489

Fragments arranged by size:

641 624 489 371 134

BanII G_rGCy'C

Cuts at: 0 475 2259

Size: 475 1784

BccI CCATC

Cuts at: 0 81 197 233 530 842 956 1025 1229

Size: 81 116 36 297 312 114 69 204

Cuts at: 1229 1769 2048 2259

Size: 540 279 211

Fragments arranged by size:

540 312 297 279 211 204 116 114 81 69 36

BceII ACGGCnnnnnnnnnn'n_

Cuts at: 0 1060 1075 1333 2259

Size: 1060 15 258 926

Fragments arranged by size:

1060 926 258 15

BcgI CGAnnnnnnTGCnnnnnnnnnn_nn'

Cuts at: 0 367 401 2259

Size: 367 34 1858

Fragments arranged by size:

1858 367 34

BfiI ACTGGG

Cuts at: 0 456 1823 2259

Size: 456 1367 436

Fragments arranged by size:

1367 456 436

BglI GCCn_nnn'nGGC

Cuts at: 0 201 394 1768 2259

Size: 201 193 1374 491

Fragments arranged by size:

1374 491 201 193

FIG. 19B

BglII A'GATC_T

Cuts at: 0 286 2259

Size: 286 1973

BmgI GkGCCC

Cuts at: 0 518 1592 2259

Size: 518 1074 667

Fragments arranged by size:

1074 667 518

BplI GAGnnnnnCTC

Cuts at: 0 171 2259

Size: 171 2088

BpmI CTGGAGnnnnnnnnnnnnnnnn'_nn'

Cuts at: 0 462 2259

Size: 462 1797

Bpu10I CC'TnA_GC

Cuts at: 0 469 2149 2259

Size: 469 1680 110

Fragments arranged by size:

1680 469 110

BsaI GGTCTCn'nnnn_

Cuts at: 0 1531 1841 1941 2259

Size: 1531 310 100 318

Fragments arranged by size:

1531 318 310 100

BsaWI w'CCGG_w

Cuts at: 0 621 1939 2116 2259

Size: 621 1318 177 143

Fragments arranged by size:

1318 621 177 143

BsbI CAACAC

Cuts at: 0 1332 1560 1696 1975 2259

Size: 1332 228 136 279 284

Fragments arranged by size:

1332 284 279 228 136

BscGI CCCGT

Cuts at: 0 294 1011 2166 2259

Size: 294 717 1155 93

Fragments arranged by size:

1155 717 294 93

BseRI GAGGAGnnnnnnnn'_nn'

Cuts at: 0 1116 2151 2259

Size: 1116 1035 108

Fragments arranged by size:

1116 1035 108

FIG. 19C

FIG. 19D

BspGI CTGGAC
Cuts at: 0 1098 1190 2259
Size: 1098 92 1069
Fragments arranged by size:
1098 1069 92

BspMI ACCTGCnnnn'nnnn
Cuts at: 0 394 703 2259
Size: 394 309 1556
Fragments arranged by size:
1556 394 309

BsrI ACTG_Gn'
Cuts at: 0 119 257 459 756 860 1822 2259
Size: 119 138 202 297 104 962 437
Fragments arranged by size:
962 437 297 202 138 119 104

BsrDI GCAATG_nn'
Cuts at: 0 1571 2259
Size: 1571 688

BsrFI r'CCGG_y
Cuts at: 0 272 442 1117 2259
Size: 272 170 675 1142
Fragments arranged by size:
1142 675 272 170

BssSI C'TCGT_G
Cuts at: 0 2251 2259
Size: 2251 8

BstXI CCAn_nnnn'nTGG
Cuts at: 0 909 2259
Size: 909 1350

BstYI r'GATC_y
Cuts at: 0 286 970 1536 2259
Size: 286 684 566 723
Fragments arranged by size:
723 684 566 286

Bsu36I CC'TnA_GG
Cuts at: 0 1035 2209 2259
Size: 1035 1174 50
Fragments arranged by size:
1174 1035 50

Cac8I GCn'nGC
Cuts at: 0 1069 1119 1250 1439 1461 1888 2133 2193
Size: 1069 50 131 189 22 427 245 60
Cuts at: 2193 2259
Size: 66
Fragments arranged by size:
1069 427 245 189 131 66 60 50

FIG. 19E

CjeI ACnnnnnnTGnnnnnnnnnnnnnnn
 Cuts at: 0 64 164 242 410 530 585 855 1526
 Size: 64 100 78 168 120 55 270 671
 Cuts at: 1526 2259
 Size: 733
 Fragments arranged by size:
 733 671 270 168 120 100 78 64 55
 CviRI TG'CA
 Cuts at: 0 160 562 641 1156 1183 1322 1486 1551
 Size: 160 402 79 515 27 139 164 65
 Cuts at: 1551 2259
 Size: 708
 Fragments arranged by size:
 708 515 402 164 160 139 79 65 27
 DpnI GA'TC
 Cuts at: 0 288 972 1538 2030 2259
 Size: 288 684 566 492 229
 Fragments arranged by size:
 684 566 492 288 229
 DraIII CAC_nnn'GTG
 Cuts at: 0 1557 2259
 Size: 1557 702
 DrdI GACnn_nn'nnGTC
 Cuts at: 0 1185 2259
 Size: 1185 1074
 DrdII GAACCA
 Cuts at: 0 364 1285 2259
 Size: 364 921 974
 Fragments arranged by size:
 974 921 364
 DsaI C'CryG_G
 Cuts at: 0 1090 1348 1453 2259
 Size: 1090 258 105 806
 Fragments arranged by size:
 1090 806 258 105
 EaeI y'GGCC_r
 Cuts at: 0 270 490 2259
 Size: 270 220 1769
 Fragments arranged by size:
 1769 270 220

FIG. 19F

EagI C'GGCC_G
Cuts at: 0 270 2259
Size: 270 1989

EarI CTCTTCn'nnn_
Cuts at: 0 15 295 1711 2259
Size: 15 280 1416 548
Fragments arranged by size:
1416 548 280 15

EcoNI CCTnn'n_nnAGG
Cuts at: 0 67 2208 2259
Size: 67 2141 51
Fragments arranged by size:
2141 67 51

EcoO109I rG'GnC_Cy
Cuts at: 0 791 932 1031 2145 2259
Size: 791 141 99 1114 114
Fragments arranged by size:
1114 791 141 114 99

EcoRI G'AATT_C
Cuts at: 0 1497 2259
Size: 1497 762

FauI CCCGCnnnn'nn_
Cuts at: 0 26 1241 2086 2140 2259
Size: 26 1215 845 54 119
Fragments arranged by size:
1215 845 119 54 26

FokI GGATGnnnnnnnnn'nnnn_
Cuts at: 0 1011 1239 1434 1671 2218 2259
Size: 1011 228 195 237 547 41
Fragments arranged by size:
1011 547 237 228 195 41

FspI TGC'GCA
Cuts at: 0 524 1110 2259
Size: 524 586 1149
Fragments arranged by size:
1149 586 524

GdiII y'GGCC_G
Cuts at: 0 270 2259
Size: 270 1989

HaeI wGG'CCw
Cuts at: 0 397 492 1164 2259
Size: 397 95 672 1095
Fragments arranged by size:
1095 672 397 95

FIG. 19G

HgiEI ACCnnnnnnnGGT

Cuts at: 0 230 2259

Size: 230 2029

HhaI G₋CG'C

Cuts at: 0 525 1064 1089 1111 2259

Size: 525 539 25 22 1148

Fragments arranged by size:

1148 539 525 25 22

Hin4I GAbnnnnnvTC

Cuts at: 0 83 171 1235 1541 1791 2259

Size: 83 88 1064 306 250 468

Fragments arranged by size:

1064 468 306 250 88 83

HincII GTy'rAC

Cuts at: 0 1469 2259

Size: 1469 790

HinfI G'AnT₋C

Cuts at: 0 305 987 2173 2259

Size: 305 682 1186 86

Fragments arranged by size:

1186 682 305 86

HphI GGTGAnnnnnnn₋n'

Cuts at: 0 1373 1797 2259

Size: 1373 424 462

Fragments arranged by size:

1373 462 424

MaeIII 'GTnAC₋

Cuts at: 0 221 433 862 1617 1679 1784 1803 2039

Size: 221 212 429 755 62 105 19 236

Cuts at: 2039 2259

Size: 220

Fragments arranged by size:

755 429 236 221 220 212 105 62 19

MboII GAAGAnnnnnnn₋n'

Cuts at: 0 2 151 312 353 491 980 1728 1912

Size: 2 149 161 41 138 489 748 184

Cuts at: 1912 2259

Size: 347

Fragments arranged by size:

748 489 347 184 161 149 138 41

2

FIG. 19H

MscI TGG'CCA

Cuts at: 0 492 2259

Size: 492 1767

MslI CAynn'nnrTG

Cuts at: 0 1422 1452 2259

Size: 1422 30 807

Fragments arranged by size:

1422 807 30

MspAII CmG'CkG

Cuts at: 0 282 557 1050 2181 2259

Size: 282 275 493 1131 78

Fragments arranged by size:

1131 493 282 275 78

MwoI GCnn_nnn'nnGC

Cuts at: 0 201 210 394 470 810 1068 1135 1138

Size: 201 9 184 76 340 258 67 3

Cuts at: 1138 1650 1768 2259

Size: 512 118 491

Fragments arranged by size:

512 491 340 258 201 184 118 76 67 9 3

NciI CC's_GG

Cuts at: 0 192 413 714 788 789 1534 1625 1920

Size: 192 221 301 74 1 745 91 295

Cuts at: 1920 2259

Size: 339

Fragments arranged by size:

745 339 301 295 221 192 91 74 1

NcoI C'CATG_G

Cuts at: 0 1453 2259

Size: 1453 806

NgoAIV G'CCGG_C

Cuts at: 0 1117 2259

Size: 1117 1142

NlaIII _CATG'

Cuts at: 0 5 155 804 1457 1830 2105 2259

Size: 5 150 649 653 373 275 154

Fragments arranged by size:

653 649 373 275 154 150 5

FIG. 19I

PflMI CCA_nnnn'nTGG
 Cuts at: 0 1577 2259
 Size: 1577 682
 Psp5II rG'GwC_Cy
 Cuts at: 0 791 932 2259
 Size: 791 141 1327
 Fragments arranged by size:
 1327 791 141
 PstI C_TGCA'G
 Cuts at: 0 1158 2259
 Size: 1158 1101
 PvuII CAG'CTG
 Cuts at: 0 557 2181 2259
 Size: 557 1624 78
 Fragments arranged by size:
 1624 557 78
 RcaI T'CATG_A
 Cuts at: 0 2101 2259
 Size: 2101 158
 RsaI GT'AC
 Cuts at: 0 261 680 999 1014 2259
 Size: 261 419 319 15 1245
 Fragments arranged by size:
 1245 419 319 261 15
 SanDI GG'GwC_CC
 Cuts at: 0 791 2259
 Size: 791 1468
 SapI GCTCTTCn'nnn_
 Cuts at: 0 15 2259
 Size: 15 2244
 Sau3AI 'GATC_
 Cuts at: 0 286 970 1536 2028 2259
 Size: 286 684 566 492 231
 Fragments arranged by size:
 684 566 492 286 231
 SfaNI GCATCnnnnn'nnnn_
 Cuts at: 0 206 938 1192 1202 2259
 Size: 206 732 254 10 1057
 Fragments arranged by size:
 1057 732 254 206 10
 SfcI C'TryA_G
 Cuts at: 0 334 427 1154 2259
 Size: 334 93 727 1105
 Fragments arranged by size:
 1105 727 334 93

FIG. 19J

SmaI CCC'GGG
 Cuts at: 0 789 2259
 Size: 789 1470
 Sse8647I AG'GwC_CT
 Cuts at: 0 932 2259
 Size: 932 1327
 SspI AAT'ATT
 Cuts at: 0 2022 2259
 Size: 2022 237
 StuI AGG'CCT
 Cuts at: 0 397 2259
 Size: 397 1862
 StyI C'CwwG_G
 Cuts at: 0 398 1453 1997 2259
 Size: 398 1055 544 262
 Fragments arranged by size:
 1055 544 398 262
 TaqI T'CG_A
 Cuts at: 0 77 377 749 2259
 Size: 77 300 372 1510
 Fragments arranged by size:
 1510 372 300 77
 TauI GCsGC
 Cuts at: 0 116 202 270 1065 2259
 Size: 116 86 68 795 1194
 Fragments arranged by size:
 1194 795 116 86 68
 TfiI G'AwT_C
 Cuts at: 0 305 987 2173 2259
 Size: 305 682 1186 86
 Fragments arranged by size:
 1186 682 305 86
 ThaI CG'CG
 Cuts at: 0 201 1064 2259
 Size: 201 863 1195
 Fragments arranged by size:
 1195 863 201
 Tsp45I 'GTsAC_
 Cuts at: 0 221 862 1679 1784 1803 2039 2259
 Size: 221 641 817 105 19 236 220
 Fragments arranged by size:
 817 641 236 221 220 105 19

FIG. 19K

Tsp509I 'AATT_
 Cuts at: 0 495 1488 1497 1731 2244 2259
 Size: 495 993 9 234 513 15
 Fragments arranged by size:
 993 513 495 234 15 9

Tth111I GACn'n_nGTC
 Cuts at: 0 49 2259
 Size: 49 2210

Tth111II CAACAnnnnnnnnnn_nn'
 Cuts at: 0 234 577 675 1452 1922 2259
 Size: 234 343 98 777 470 337
 Fragments arranged by size:
 777 470 343 337 234 98

UbaCI wGTACw
 Cuts at: 0 261 680 2259
 Size: 261 419 1579
 Fragments arranged by size:
 1579 419 261

XcmI CCAnnnn_n'nnnnTGG
 Cuts at: 0 396 1829 2259
 Size: 396 1433 430
 Fragments arranged by size:
 1433 430 396

XmnI GAAnn'nnTTC
 Cuts at: 0 9 348 2259
 Size: 9 339 1911
 Fragments arranged by size:
 1911 339 9

Enzymes that do cut and were not excluded:

AceIII	AlwI	AlwNI	ApaLI	ApoI	AvaI	AvaII	BaeI
BamHI	BanI	BanII	BccI	Bcefi	BcgI	BfiI	BglI
BglII	BmgI	BpII	BpmI	Bpu10I	BsaI	BsaWI	Bsbl
BscGI	BseRI	BsgI	BsiEI	BsiHKAII	BsII	BsmI	BsmAI
BsmFI	Bsp24I	Bsp1286I	BspGI	BspMI	BsrI	BsrDI	BsrFI
BssSI	BstXI	BstYI	Bsu36I	Cac8I	CjeI	CviRI	DpnI
DraIII	DrdI	DrdII	DsaI	EaeI	EagI	EarI	EcoNI
EcoO109I	EcoRI	FauI	FokI	FspI	GdiII	HaeI	HgiEII
HhaI	Hin4I	HincII	HinfI	HphI	MaeIII	MboII	MscI
MslII	MspAII	MwoI	NciI	NcoI	NgoAIV	NlaIII	PfiMI
Psp5II	PstI	PvuII	RcaI	RsaI	SanDI	SapI	Sau3AI
SfaNI	SfcI	SmaI	Sse8647I	SspI	StuI	StyI	TaqI
TauI	TfiI	ThaI	Tsp45I	Tsp509I	Tth111I	Tth111II	UbaCI
XcmI	XmnI						

FIG. 19L

Enzymes that do not cut:

AatII	AccI	AflII	AflIII	AhdI	ApaI	ApaBI	AscI
AvrII	BbsI	Bce83I	BclI	BfaI	Bpu1102I	BsaAI	BsaBI
BsaHI	BsaXI	BsmBI	BspEI	BspLU11I	BsrBI	BsrGI	BssHII
Bst1107I	BstEII	ClaI	DraI	EciI	Eco47III	Eco57I	EcoRV
FseI	HaeII	HgaI	HindIII	HpaI	KpnI	MaeII	MluI
MmeI	MseI	MunI	NarI	NdeI	NheI	NotI	NruI
NsiI	NspI	NspV	PacI	Pfl1108I	PinAI	PleI	PmeI
PmlI	PshAI	Psp1406I	PvuI	RleAI	RsrII	SacI	SacII
Sall	ScaI	SexAI	SfiI	SgfI	SgrAI	SnaBI	SpeI
SphI	SrfI	Sse8387I	SunI	Swal	TaqII	TaqII	VspI
XbaI	XhoI						

Enzymes excluded; MinCuts: 1 MaxCuts: 10

AcII	AluI	BbvI	BsaII	BsoFI	CjeI	CjePI	CjePI
CviII	DdeI	EcoRII	HaeIII	MnlI	MspI	NlaIV	Sau96I
ScrFI	TseI	TspRI					

FIG. 19M

(Linear) MAPSORT of: bovlactof.gb_om check: 2217 from: 1 to: 2351
 LOCUS BOVLACTOF 2351 bp ss-mRNA MAM
 DEFINITION Bovine lactoferrin mRNA, complete cds.
 ACCESSION M63502
 KEYWORDS lactoferrin.
 SOURCE B.taurus, cDNA to mRNA.
 ORGANISM Bos taurus . . .
 Mismatch: 0 MinCuts = 1 MaxCuts: 10
 With 209 enzymes: *

AceIII CAGCTCnnnnnnnn'nnnn_
 Cuts at: 0 494 526 969 1553 1841 2216 2351
 Size: 494 32 443 584 288 375 135
 Fragments arranged by size:
 584 494 443 375 288 135 32

AflIII A'CryG_T
 Cuts at: 0 1913 2351
 Size: 1913 438

AhdI GACnn_n'nnGTC
 Cuts at: 0 1460 2351
 Size: 1460 891

AlwI GGATCnnnn'n_
 Cuts at: 0 480 1019 1032 2351
 Size: 480 539 13 1319
 Fragments arranged by size:
 1319 539 480 13

AlwNI CAG_nnn'CTG
 Cuts at: 0 1600 1631 1928 1946 2351
 Size: 1600 31 297 18 405
 Fragments arranged by size:
 1600 405 297 31 18

ApoI r'AATT_y
 Cuts at: 0 549 1442 1551 2351
 Size: 549 893 109 800
 Fragments arranged by size:
 893 800 549 109

AvaI C'yCGr_G
 Cuts at: 0 101 522 652 2351
 Size: 101 421 130 1699
 Fragments arranged by size:
 1699 421 130 101

FIG. 20A

AvaII G'GwC_C
Cuts at: 0 305 416 460 770 845 986 1149 2244
Size: 305 111 44 310 75 141 163 1095
Cuts at: 2244 2351
Size: 107
Fragments arranged by size:
1095 310 305 163 141 111 107 75 44

BamHI G'GATC_C
Cuts at: 0 1024 2351
Size: 1024 1327

BanI G'GyrC_C
Cuts at: 0 678 806 1319 1393 1690 1824 2351
Size: 678 128 513 74 297 134 527
Fragments arranged by size:
678 527 513 297 134 128 74

BanII G_rGCy'C
Cuts at: 0 80 529 1062 1435 2351
Size: 80 449 533 373 916
Fragments arranged by size:
916 533 449 373 80

BbsI GAAGACnn'nnnn_
Cuts at: 0 895 2351
Size: 895 1456

BbvI GCAGCnnnnnnnn'nnnn_
Cuts at: 0 83 342 409 412 1842 1915 1920 2351
Size: 83 259 67 3 1430 73 5 431
Fragments arranged by size:
1430 431 259 83 73 67 5 3

BccI CCATC
Cuts at: 0 120 128 162 278 881 1283 1823 2351
Size: 120 8 34 116 603 402 540 528
Fragments arranged by size:
603 540 528 402 120 116 34 8

Bce83I CTTGAGnnnnnnnnnnnnnn'_nn'
Cuts at: 0 524 2351
Size: 524 1827

BceII ACGGCnnnnnnnnnnnn'n_
Cuts at: 0 370 1129 1231 1387 1462 2113 2351
Size: 370 759 102 156 75 651 238
Fragments arranged by size:
759 651 370 238 156 102 75

BfaI C'TA_G
Cuts at: 0 1365 2183 2351
Size: 1365 818 168
Fragments arranged by size:
1365 818 168

FIG. 20B

BfiI ACTGGG
 Cuts at: 0 1776 2351
 Size: 1776 575
 BglI GCCn_nnn'nGGC
 Cuts at: 0 448 1578 1822 2351
 Size: 448 1130 244 529
 Fragments arranged by size:
 1130 529 448 244
 BglII A'GATC_T
 Cuts at: 0 337 2351
 Size: 337 2014
 BmgI GkGCCC
 Cuts at: 0 1572 1646 2351
 Size: 1572 74 705
 Fragments arranged by size:
 1572 705 74
 BpmI CTGGAGnnnnnnnnnnnnnnn_nn'
 Cuts at: 0 516 727 2216 2351
 Size: 516 211 1489 135
 Fragments arranged by size:
 1489 516 211 135
 Bpu10I CC'TnA_GC
 Cuts at: 0 1699 2202 2351
 Size: 1699 503 149
 Fragments arranged by size:
 1699 503 149
 BsaI GGTCTCn'nnnn_
 Cuts at: 0 1373 2351
 Size: 1373 978
 BsaAI yAC'GTr
 Cuts at: 0 1916 2351
 Size: 1916 435
 BsaHI Gr'CG_yC
 Cuts at: 0 32 807 1218 2351
 Size: 32 775 411 1133
 Fragments arranged by size:
 1133 775 411 32
 BsaWI w'CCGG_w
 Cuts at: 0 15 1339 2351
 Size: 15 1324 1012
 Fragments arranged by size:
 1324 1012 15
 BsaXI ACnnnnnnCTCC
 Cuts at: 0 634 1058 2351
 Size: 634 424 1293
 Fragments arranged by size:
 1293 634 424

FIG. 20C

BsbI CAACAC

Cuts at: 0 2029 2351

Size: 2029 322

BscGI CCCGT

Cuts at: 0 449 498 702 2351

Size: 449 49 204 1649

Fragments arranged by size:

1649 449 204 49

BseRI GAGGAGnnnnnnnn_nn'

Cuts at: 0 638 1119 1170 2198 2351

Size: 638 481 51 1028 153

Fragments arranged by size:

1028 638 481 153 51

BsiHKA I G_wGCw'C

Cuts at: 0 191 1767 2351

Size: 191 1576 584

Fragments arranged by size:

1576 584 191

BsmAI GTCTCn'nnnn_

Cuts at: 0 361 703 723 949 1373 1897 2351

Size: 361 342 20 226 424 524 454

Fragments arranged by size:

524 454 424 361 342 226 20

BsmBI CGTCTCn'nnnn_

Cuts at: 0 703 723 2351

Size: 703 20 1628

Fragments arranged by size:

1628 703 20

BsoFI GC'n_GC

Cuts at: 0 97 155 321 331 401 423 1193 1856

Size: 97 58 166 10 70 22 770 663

Cuts at: 1856 1909 1929 2351

Size: 53 20 422

Fragments arranged by size:

770 663 422 166 97 70 58 53 22 20 10

Bsp24I GACnnnnnnTGnnnnnnnn_nnnnn'

Cuts at: 0 76 108 260 292 590 622 882 914

Size: 76 32 152 32 298 32 260 32

Cuts at: 914 1725 1757 2351

Size: 811 32 594

Fragments arranged by size:

811 594 298 260 152 76 32 32 32 32 32

FIG. 20D

Bsp1286I G_dGCh'C
 Cuts at: 0 80 191 529 1062 1435 1574 1648 1767
 Size: 80 111 338 533 373 139 74 119
 Cuts at: 1767 2351
 Size: 584
 Fragments arranged by size:
 584 533 373 338 139 119 111 80 74
 BspEI T'CCGG_A
 Cuts at: 0 15 2351
 Size: 15 2336
 BspGI CTGGAC
 Cuts at: 0 416 511 1634 2351
 Size: 416 95 1123 717
 Fragments arranged by size:
 1123 717 416 95
 BspMI ACCTGCnnnn'nnnn_
 Cuts at: 0 448 997 2351
 Size: 448 549 1354
 Fragments arranged by size:
 1354 549 448
 BsrI ACTG_Gn'
 Cuts at: 0 324 635 773 810 1779 2351
 Size: 324 311 138 37 969 572
 Fragments arranged by size:
 969 572 324 311 138 37
 BsrBI GAG'CGG
 Cuts at: 0 1192 2351
 Size: 1192 1159
 BsrDI GCAATG_nn'
 Cuts at: 0 2101 2351
 Size: 2101 250
 BstXI CCA_nnnn'nTGG
 Cuts at: 0 963 2351
 Size: 963 1388
 BstYI r'GATC_y
 Cuts at: 0 337 1024 2351
 Size: 337 687 1327
 Fragments arranged by size:
 1327 687 337
 Bsu36I CC'TnA_GG
 Cuts at: 0 1089 1153 2351
 Size: 1089 64 1198
 Fragments arranged by size:
 1198 1089 64

FIG. 20E

CviRI TG'CA

Cuts at: 0 425 577 616 695 1237 1491 1770 2174

Size: 425 152 39 79 542 254 279 404

Cuts at: 2174 2351

Size: 177

Fragments arranged by size:

542 425 404 279 254 177 152 79 39

DpnI GA'TC

Cuts at: 0 339 474 897 1026 1518 2351

Size: 339 135 423 129 492 833

Fragments arranged by size:

833 492 423 339 135 129

DraIII CAC_nnn'GTG

Cuts at: 0 1886 2035 2351

Size: 1886 149 316

Fragments arranged by size:

1886 316 149

DrdI GACnn_nn'nnGTC

Cuts at: 0 353 1239 2351

Size: 353 886 1112

Fragments arranged by size:

1112 886 353

DrdII GAACCA

Cuts at: 0 146 634 659 2351

Size: 146 488 25 1692

Fragments arranged by size:

1692 488 146 25

DsaI C'CryG_G

Cuts at: 0 1144 1213 1402 1477 1507 2351

Size: 1144 69 189 75 30 844

Fragments arranged by size:

1144 844 189 75 69 30

EaeI y'GGCC_r

Cuts at: 0 321 382 977 1193 2041 2098 2351

Size: 321 61 595 216 848 57 253

Fragments arranged by size:

848 595 321 253 216 61 57

FIG. 20F

FIG. 20G

FspI TGC'GCA

Cuts at: 0 1541 2351

Size: 1541 810

GdiII y'GGCC_G

Cuts at: 0 321 382 977 1193 2098 2351

Size: 321 61 595 216 905 253

Fragments arranged by size:

905 595 321 253 216 61

HaeI wGG'CCw

Cuts at: 0 1315 2043 2351

Size: 1315 728 308

Fragments arranged by size:

1315 728 308

HaeII r_GCGC'y

Cuts at: 0 810 1050 2351

Size: 810 240 1301

Fragments arranged by size:

1301 810 240

HgaI GACGCnnnnn'nnnnn

Cuts at: 0 40 1207 2351

Size: 40 1167 1144

Fragments arranged by size:

1167 1144 40

HgiII ACCnnnnnnGGT

Cuts at: 0 275 2351

Size: 275 2076

HhaI G_CG'C

Cuts at: 0 809 920 1049 1118 1542 2151 2239 2351

Size: 809 111 129 69 424 609 88 112

Fragments arranged by size:

809 609 424 129 112 111 88 69

Hin4I GAbnnnnnvTC

Cuts at: 0 1289 1459 1588 1845 2351

Size: 1289 170 129 257 506

Fragments arranged by size:

1289 506 257 170 129

HincII GTy'rAC

Cuts at: 0 609 1523 2351

Size: 609 914 828

Fragments arranged by size:

914 828 609

FIG. 20H

HindIII A'AGCT_T
 Cuts at: 0 903 2351
 Size: 903 1448

HinfI G'AnT_C
 Cuts at: 0 19 354 487 516 1002 1041 1597 1790
 Size: 19 335 133 29 486 39 556 193
 Cuts at: 1790 1877 2351
 Size: 87 474
 Fragments arranged by size:
 556 486 474 335 193 133 87 39 29 19

HphI GGTGAnnnnnnn_n'
 Cuts at: 0 191 1121 2351
 Size: 191 930 1230
 Fragments arranged by size:
 1230 930 191

KpnI G_GTAC'C
 Cuts at: 0 1397 2351
 Size: 1397 954

MaeII A'CG_T
 Cuts at: 0 112 712 1201 1705 1714 1915 2064 2351
 Size: 112 600 489 504 9 201 149 287
 Fragments arranged by size:
 600 504 489 287 201 149 112 9

MaeIII 'GTnAC_
 Cuts at: 0 266 517 1202 1838 2093 2351
 Size: 266 251 685 636 255 258
 Fragments arranged by size:
 685 636 266 258 255 251

MboII GAAGAnnnnnnn_n'
 Cuts at: 0 41 188 404 545 900 1094 1175 2082
 Size: 41 147 216 141 355 194 81 907
 Cuts at: 2082 2351
 Size: 269
 Fragments arranged by size:
 907 355 269 216 194 147 141 81 41

FIG. 20I

MmeI TCCrACnnnnnnnnnnnnnnnnnnnnnnnn'nn'

Cuts at: 0 2248 2351

Size: 2248 103

MscI TGG'CCA

Cuts at: 0 2043 2351

Size: 2043 308

MseI T'TA_A

Cuts at: 0 724 2351

Size: 724 1627

MslI CAynn'nnrTG

Cuts at: 0 204 373 480 1476 1506 2351

Size: 204 169 107 996 30 845

Fragments arranged by size:

996 845 204 169 107 30

MspI C'CG_G

Cuts at: 0 16 237 302 431 653 976 1340 1678

Size: 16 221 65 129 222 323 364 338

Cuts at: 1678 1974 2351

Size: 296 377

Fragments arranged by size:

377 364 338 323 296 222 221 129 65 16

MspAII CmG'CkG

Cuts at: 0 413 422 465 565 2351

Size: 413 9 43 100 1786

Fragments arranged by size:

1786 413 100 43 9

NarI GG'CG_CC

Cuts at: 0 807 2351

Size: 807 1544

NciI CC's_GG

Cuts at: 0 238 303 653 654 976 1679 1974 2351

Size: 238 65 350 1 322 703 295 377

Fragments arranged by size:

703 377 350 322 295 238 65 1

NcoI C'CATG_G

Cuts at: 0 1507 2351

Size: 1507 844

NheI G'CTAG_C

Cuts at: 0 2182 2351

Size: 2182 169

NlaIII _CATG'

Cuts at: 0 44 287 858 1441 1511 2351

Size: 44 243 571 583 70 840

Fragments arranged by size:

840 583 571 243 70 44

FIG. 20J

PflMI CCA_nnnn'nTGG
Cuts at: 0 1631 2351
Size: 1631 720

PleI GAGTCnnnn'n
Cuts at: 0 27 362 524 996 1591 2351
Size: 27 335 162 472 595 760
Fragments arranged by size:
760 595 472 335 162 27

PmlI CAC'GTG
Cuts at: 0 1916 2351
Size: 1916 435

Psp5II rG'GwC_Cy
Cuts at: 0 305 845 986 1149 2244 2351
Size: 305 540 141 163 1095 107
Fragments arranged by size:
1095 540 305 163 141 107

Psp1406I AA'CG_TT
Cuts at: 0 112 2351
Size: 112 2239

PstI C_TGCA'G
Cuts at: 0 697 1493 1772 2351
Size: 697 796 279 579
Fragments arranged by size:
796 697 579 279

PvuII CAG'CTG
Cuts at: 0 413 422 565 2351
Size: 413 9 143 1786
Fragments arranged by size:
1786 413 143 9

RsaI GT'AC
Cuts at: 0 125 501 1053 1122 1395 1665 2351
Size: 125 376 552 69 273 270 686
Fragments arranged by size:
686 552 376 273 270 125 69

SanDI GG'GwC_CC
Cuts at: 0 305 2351
Size: 305 2046

SapI GCTCTTCn'nnn_
Cuts at: 0 54 2351
Size: 54 2297

Sau3AI 'GATC_
Cuts at: 0 337 472 895 1024 1516 2351
Size: 337 135 423 129 492 835
Fragments arranged by size:
835 492 423 337 135 129

FIG. 20K

ScaI AGT'ACT

Cuts at: 0 1665 2351

Size: 1665 686

SfaNI GCATCnnnnn'nnnn

Cuts at: 0 250 251 806 1246 1256 2351

Size: 250 1 555 440 10 1095

Fragments arranged by size:

1095 555 440 250 10 1

SfiI C'TryA_G

Cuts at: 0 693 1489 1768 2351

Size: 693 796 279 583

Fragments arranged by size:

796 693 583 279

SmaI CCC'GGG

Cuts at: 0 654 2351

Size: 654 1697

SspI AAT'ATT

Cuts at: 0 2076 2351

Size: 2076 275

StyI C'CwwG_G

Cuts at: 0 71 80 223 452 1507 2351

Size: 71 9 143 229 1055 844

Fragments arranged by size:

1055 844 229 143 71 9

TaqI T'CG_A

Cuts at: 0 116 523 1032 1819 2351

Size: 116 407 509 787 532

Fragments arranged by size:

787 532 509 407 116

TaqII GACCGAnnnnnnnnn'nn'

Cuts at: 0 174 457 2351

Size: 174 283 1894

Fragments arranged by size:

1894 283 174

TauI GCsGC

Cuts at: 0 155 321 1193 2351

Size: 155 166 872 1158

Fragments arranged by size:

1158 872 166 155

TfiI G'AwT_C

Cuts at: 0 487 1041 1790 1877 2351

Size: 487 554 749 87 474

Fragments arranged by size:

749 554 487 474 87

FIG. 20L

ThaI CG'CG

Cuts at: 0 246 1118 2239 2351

Size: 246 872 1121 112

Fragments arranged by size:

1121 872 246 112

TseI GCwGC

Cuts at: 0 97 331 401 423 1856 1909 1929 2351

Size: 97 234 70 22 1433 53 20 422

Fragments arranged by size:

1433 422 234 97 70 53 22 20

Tsp45I 'GTsAC_

Cuts at: 0 266 517 1202 1838 2093 2351

Size: 266 251 685 636 255 258

Fragments arranged by size:

685 636 266 258 255 251

Tsp509I 'AATT_

Cuts at: 0 549 1442 1551 2298 2329 2351

Size: 549 893 109 747 31 22

Fragments arranged by size:

893 747 549 109 31 22

TspRI CAGTGnn'

Cuts at: 0 171 642 742 817 1182 1232 1304 1772

Size: 171 471 100 75 365 50 72 468

Cuts at: 1772 2036 2351

Size: 264 315

Fragments arranged by size:

471 468 365 315 264 171 100 75 72 50

Tth111I GACn'n_nGTC

Cuts at: 0 88 515 1737 2351

Size: 88 427 1222 614

Fragments arranged by size:

1222 614 427 88

Tth111I CAARCAnnnnnnnnnn_nn'

Cuts at: 0 279 604 729 1368 1938 1976 2351

Size: 279 325 125 639 570 38 375

Fragments arranged by size:

639 570 375 325 279 125 38

FIG. 20M

UbaCI wGTACw

Cuts at: 0 1665 2351

Size: 1665 686

XcmI CCAnnnn_n'nnnnTGG

Cuts at: 0 450 2351

Size: 450 1901

XhoI C'TCGA_G

Cuts at: 0 522 2351

Size: 522 1829

XmnI GAAnn'nnTTC

Cuts at: 0 48 232 2351

Size: 48 184 2119

Fragments arranged by size:

2119 184 48

Enzymes that do cut and were not excluded:

AceIII	AflIII	AhdI	AlwI	AlwNI	ApoI	AvaI	AvaII
BamHI	BanI	BanII	BbsI	BbvI	BccI	Bce83I	BceII
BfaI	BfiI	BglI	BglII	BmgI	BpmI	Bpu10I	BsaI
BsaAI	BsaHI	BsaWI	BsaXI	BsbI	BscGI	BseRI	BsiHKAII
BsmAI	BsmBI	BsoFI	Bsp24I	Bsp1286I	BspEI	BspGI*	BspMI
BsrI	BsrBI	BsrDI	BstXI	BstYI	Bsu36I	CviRI	DpnI
DraIII	DrdI	DrdII	DsaI	EaeI	EarI	EciI	Eco57I
EcoNI	EcoO109I	EcoRI	FauI	FokI	FspI	GdiII	HaeI
HaeII	HgaI	Hgi	EII	HhaI	Hin4I	HincII	HindIII
HinfI	HphI	KpnI	MaeII	MaeIII	MboII	MmeI	MscI
MseI	MslI	MspI	MspAII	NarI	NciI	NcoI	NheI
NlaIII	PflMI	PleI	PmlI	Psp5II	Psp1406I	PstI	PvuII
RsaI	SanDI	SapI	Sau3AI	ScaI	SfaNI	SfcI	SmaI
SspI	StyI	TaqI	TaqII	TauI	TfiI	ThaI	TseI
Tsp45I	Tsp509I	TspRI	Tth111I	Tth111II	UbaCI	XcmI	XhoI

XmnI

Enzymes that do not cut:

AatII	AccI	AflII	Apal	ApaBI	ApaLI	AscI	AvrII
BaeI	BcgI	BcgI	BclI	BpII	Bpu1102I	BsaBI	BsgI
BsiEI	BsmI	BspLU11I	BsrFI	BsrGI	BssHII	BssSI	Bst1107I
BstEII	Clal	DraI	EagI	Eco47III	EcoRV	FseI	HpaI
MluI	MunI	NdeI	NgoAIV	NotI	NruI	NsiI	NspI
NspV	PacI	Pfl1108I	PinAI	PmeI	PshAI	PvuI	RcaI
RleAI	RsrII	SacI	SacII	Sall	SexAI	Sfil	SgfI
SgrAI	SnaBI	SpeI	SphI	SrfI	Sse8387I	Sse8647I	StuI
SunI	SwaI	VspI	XbaI				

Enzymes excluded; MinCuts: 1 MaxCuts: 10

AcI	AluI	BsaII	BsII	BsmFI	Cac8I	CjeI	CjeI
CjePI	CjePI	CviII	DdeI	EcoRII	HaeIII	MnII	MwoI
NlaIV	Sau96I	ScrFI					

FIG. 20N